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OM protein - protein search, using sw model

Run on: October 31, 1999, 07:01:30 ; Search time 13.26 Seconds  
(without alignments)  
894.928 Million cell updates/sec

Title: us-09-297-092-1  
Perfect score: 2673  
Sequence: 1 MRLPKLLTFLWYLAWLDE.....ANNVYQVDMVVEGCGR 501

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A\_Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2673	100.0	501	1 R69600	New TGF-beta famil
2	2673	100.0	501	1 W12770	Human bone morphog
3	2673	100.0	501	1 W01799	Human MP52 protein
4	2673	100.0	501	1 W11900	Human high mol. wt
5	2673	100.0	501	1 W19210	Human TGF-beta pro
6	2673	100.0	501	1 W36100	Human MP52. Mouse
7	2673	100.0	501	1 W33008	Human MP52. Mouse
8	2673	100.0	501	1 W44868	TGF-beta superfam
9	2630	98.4	501	1 R95635	Cartilage-derived
10	2400	89.8	495	1 R60022	Growth differentia
11	2133	79.8	401	1 R40800	TGF-beta-like clon
12	905.5	33.9	436	1 R95636	Cartilage-derived
13	771	28.8	321	1 R78730	Human mature VL-1
14	771	28.8	321	1 W26591	Human bone morphog
15	660	24.7	263	1 R78739	Murine mV2 protein
16	660	24.7	263	1 W26595	Murine BMP-13 homo
17	658	24.6	120	1 R78731	Murine protein MP5
18	658	24.6	388	1 R78734	Human bone morphog
19	658	24.6	120	1 W26590	Human MP52 protein
20	658	24.6	388	1 W26592	Human bone morphog
21	654	24.5	119	1 W06920	Human MP52 growth
22	654	24.5	119	1 W19846	Human bone inducin
23	606	22.7	294	1 R78729	Human bone morphog
24	606	22.7	294	1 W26589	Human bone morphog
25	595	22.3	411	1 R78740	Fusion of BMP-2 pr
26	595	22.3	411	1 W26597	BMP-2 propeptide/B
27	573	21.4	134	1 R66867	GDF-6. Growth diff
28	544	20.4	240	1 R78738	Murine mV1 protein
29	544	20.4	240	1 W26594	Murine BMP-12 homo
30	510	19.1	161	1 R65182	GDF-7 C-terminal r
31	503	18.8	129	1 W54067	Bone morphogenetic
32	449.5	16.8	396	1 R51653	Prepro human BMP2
33	443.5	16.6	396	1 R44747	Osteogenic protein
34	443.5	16.6	396	1 R85762	Human BMP2A. Anti
35	443.5	16.6	396	1 W44303	Human osteogenic p
36	443.5	16.6	396	1 W89680	Human osteogenic p
37	441.5	16.5	396	1 R47255	Pre-pro-BMP2. Morp
38	440.5	16.5	396	1 P80619	Human Bone Morphog
39	440.5	16.5	396	1 R14241	Human BMP-2A encod
40	440.5	16.5	396	1 R29281	Human pre-pro-BMP-
41	440.5	16.5	396	1 R36732	Human BMP-2. Recom
42	440.5	16.5	396	1 W15404	Human BMP-2A. Prot
43	440.5	16.5	396	1 W24849	Human bone morphog

STROUP  
091297092  
SEQ ID:1

P-selectin ligand  
BMP2A/2B fusion pr

ALIGNMENTS

RESULT 1

R59600	R69600 standard; Protein; 501 AA.
ID	R69600;
AC	10-OCT-1995 (first entry)
DE	New TGF-beta family member - MP-52 protein sequence.
KW	Transforming growth factor-beta family; mitogenic; differentiation;
KW	treatment; prevention; disease; bone; cartilage; connective tissue;
KW	skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
KW	tissue regeneration; arthritis; ss.
OS	Homo sapiens.
FT	key
FT	peptide
FT	382
FT	/label= mature protein
PN	W09504819-A.
PD	16-FEB-1995.
PF	09-AUG-1994; E02630.
PR	10-AUG-1993; DE-326829.
PR	25-MAY-1994; DE-418222.
PR	09-JUN-1994; DE-420157.
PA	(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PI	Hotten G, Neidhardt H, Paulista M, Hoetten G;
DR	WPI; 95-090897/12.
DR	N-PSDB; Q83695.
PT	New DNA encoding a new member of the TGF beta family - and
PT	related vectors, host cells etc., has mitogenic and
PT	differentiation inducing activity, e.g. for treating or
PT	preventing diseases of bone and cartilage etc.
PS	Claim 6; Page 36; 51pp; German.
CC	The amino acid sequence of a novel member of the transforming growth
CC	factor-beta (TGF-b) family named MP-52. The gene encodes a protein
CC	of 501 amino acids (AA). The protein, or at least the mature protein,
CC	has mitogenic and/or differentiation inducing properties useful in
CC	the treatment or prevention of diseases of bone, cartilage, connective
CC	tissue, skin, mucosa, epithelium or dental tissue. The protein can also
CC	be used for wound healing and tissue regeneration e.g. in osteoporosis
CC	and arthritis.
SQ	Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;

Best Local Similarity 100.0%; Pred. No. 1.6e-191;

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps

QY	1	MRLPKLLTFLWYLAWLDE	ICTVLGAPDLGQRPGQTRGLAKAEKAPPLARNVFRP	60
Db	1	MRLPKLLTFLWYLAWLDE	ICTVLGAPDLGQRPGQTRGLAKAEKAPPLARNVFRP	60
QY	61	GGHSYGGGATNANARAGGTG	GTGGLTPQKDEPKLPPRPGGPEPKPGHPPTQATAR	120
Db	61	GGHSYGGGATNANARAGGTG	GTGGLTPQKDEPKLPPRPGGPEPKPGHPPTQATAR	120
QY	121	TVTPKGOLPGGKAPPKAGSV	PSFLKKAREPGPPPEPKPEPPPTTPEYMLSLVRL	180
Db	121	TVTPKGOLPGGKAPPKAGSV	PSFLKKAREPGPPPEPKPEPPPTTPEYMLSLVRL	180
QY	181	SDADRKGGNSVSKLEAGLAN	TITSFDKGDDRGVPVVRKQYVFDISALEKDLGLGAE	240
Db	181	SDADRKGGNSVSKLEAGLAN	TITSFDKGDDRGVPVVRKQYVFDISALEKDLGLGAE	240
QY	241	ILRKPSDTAKPAAPGCGRAA	QLKSSCPSGROPASLLDVRSPGLDGSWEVFDIWKLF	300
Db	241	ILRKPSDTAKPAAPGCGRAA	QLKSSCPSGROPASLLDVRSPGLDGSWEVFDIWKLF	300
QY	301	RNFKNSAQLCLEAWERGRAV	DVLRLGLGFDRAAROVHEKALFLVFGRTKRDLPFNEI	360
Db	301	RNFKNSAQLCLEAWERGRAV	DVLRLGLGFDRAAROVHEKALFLVFGRTKRDLPFNEI	360

Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVGRTRKKDLFFNEIKA 360  
 QY 361 RSGQDDKTVEYLFSSRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420  
 Db 361 RSGQDDKTVEYLFSSRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420  
 QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 Db 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 QY 481 SANNVYKQYEDMVVESCGR 501  
 Db 481 SANNVYKQYEDMVVESCGR 501  
 RESULT 2  
 ID W12770 standard; Protein; 501 AA.  
 AC W12770:  
 DT 11-MAY-1997 (first entry)  
 DE Human bone morphogenic factor MP52 Arg.  
 KW Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;  
 KW connective tissue; mucous membrane; epithelium; teeth;  
 KW wound healing; vulnary; tissue regeneration; osteoporosis;  
 KW bone fracture; dental implant; osteoblast.  
 OS Homo sapiens.  
 FH Key  
 FT peptide  
 FT 1. .27  
 FT /label= Sig\_peptide  
 FT cleavage\_site  
 FT 380. .381  
 FT /note= "sequencing suggests MP52 Arg is processed  
 FT proteolytically at Arg380-Arg381"  
 FT cleavage\_site  
 FT 381. .382  
 FT /note= "alternative cleavage site at Arg381-Ala382"  
 FT mat\_protein  
 FT 381. .501  
 FT /label= Mat\_protein  
 FT /note= "mature MP52 Arg preferred for use in  
 FT compns. of the invention"  
 FT  
 PN W09706254-A1.  
 PD 20-FEB-1997.  
 PF 02-AUG-1996; E03427.  
 PR 03-AUG-1995; EP-112241.  
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.  
 PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;  
 DR WPI: 97-154261/14.  
 DR N-PSDB; T59729.  
 PT New human bone morphogenic factor, MP52 Arg - used in the treatment  
 PT of osteoporosis and bone fracture, and for promoting bone regrowth  
 PS Claim 1: Page 12-15; 26pp; English.  
 CC Novel human bone morphogenic factor MP52 Arg (W12770) is a growth  
 CC factor that induces formation of cartilage from undifferentiated  
 CC mesenchymal cells and which stimulates the differentiation and  
 CC maturation of osteoblasts. It is effective for treating/preventing  
 CC bone diseases caused by abnormal bone metabolism such as  
 CC osteoporosis. It also accelerates the healing of bone fractures,  
 CC and is useful for orthopaedic reconstruction, bone transplantation,  
 CC and dental therapeutics because of its bone morphogenetic activity.  
 CC It is also effective for preventing/treating cartilage, skin,  
 CC connective tissue, mucous membrane, teeth and epithelial disorders.  
 CC Recombinant Mp52 Arg can be produced in host (e.g. CHO) cells  
 CC utilising an isolated DNA sequence (T59729) in plasmid pMS599.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEFFICTVLGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60  
 Db 1 MRLPKLLTFLWYLAWLDEFFICTVLGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60  
 QY 61 GGHSGGGATNANARAKGGTGTGGLTOPKKDEPKKLPFRPGGPEPKGHPPTQRTQATAR 120

Db 61 GGHSGGGATNANARAKGGTGTGGLTOPKKDEPKKLPFRPGGPEPKGHPPTQRTQATAR 120  
 QY 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPIIPHEYMLSLYRTL 180  
 Db 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPIIPHEYMLSLYRTL 180  
 QY 181 SDADRKGNSSVKLEAGLANITTSFDKGQDDRGVVRKQRYVFDISALEKDLGLGAEUR 240  
 Db 181 SDADRKGNSSVKLEAGLANITTSFDKGQDDRGVVRKQRYVFDISALEKDLGLGAEUR 240  
 QY 241 ILRKKPSTAKPAAPGGGAAQLKLSSCPGROPASLLDVRSPCLDGSGEVEFDIWKLF 300  
 Db 241 ILRKKPSTAKPAAPGGGAAQLKLSSCPGROPASLLDVRSPCLDGSGEVEFDIWKLF 300  
 QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVGRTRKKDLFFNEIKA 360  
 Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVGRTRKKDLFFNEIKA 360  
 QY 361 RSGQDDKTVEYLFSSRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420  
 Db 361 RSGQDDKTVEYLFSSRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420  
 QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 Db 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 QY 481 SANNVYKQYEDMVVESCGR 501  
 Db 481 SANNVYKQYEDMVVESCGR 501.  
 RESULT 3  
 ID W01799 standard; Protein; 501 AA.  
 AC W01799:  
 DT 15-OCT-1997 (first entry)  
 DE Human MP52 protein.  
 KW Human; MP52; transforming growth factor; TGF; beta; medicament;  
 KW treatment; prevention; nervous system; disease; neuropathology;  
 KW ageing.  
 OS Homo sapiens.  
 PN DE19525416-A1.  
 PD 16-JAN-1997.  
 PF 12-JUL-1995; 025416.  
 PR 12-JUL-1995; DE-025416.  
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.  
 PI Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K;  
 DR WPI: 97-078343/08.  
 DR N-PSDB; T59405.  
 PT Medicaments contg. protein MP52 - useful for treating neurological  
 PT disorders  
 PS Claim 2: Pages 12-14; 21pp; German.  
 CC The present sequence is the human Mp52 protein, which is  
 CC described in WO 9316099 and 9504819 as a member of the human  
 CC transforming growth factor beta superfamily. Active MP52 can be  
 CC used in a medicament to treat and prevent nervous system diseases,  
 CC and/or to treat neuropathological conditions caused by nervous  
 CC system ageing.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEFFICTVLGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60  
 Db 1 MRLPKLLTFLWYLAWLDEFFICTVLGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60  
 QY 61 GGHSGGGATNANARAKGGTGTGGLTOPKKDEPKKLPFRPGGPEPKGHPPTQRTQATAR 120  
 Db 61 GGHSGGGATNANARAKGGTGTGGLTOPKKDEPKKLPFRPGGPEPKGHPPTQRTQATAR 120

QY 121 TVTPKGLPGKAPPKAGSVSSFLKKAREPGPREKPPPPITPHEYMLSYRTL 180  
 DB 121 TVTPKGLPGKAPPKAGSVSSFLKKAREPGPREKPPPPITPHEYMLSYRTL 180  
 QY 181 SDADKGGNSSVKLEAGLANITTSFIDKQDDRGVVRKQRYVFDISALEKDGLLGAELR 240  
 DB 181 SDADKGGNSSVKLEAGLANITTSFIDKQDDRGVVRKQRYVFDISALEKDGLLGAELR 240  
 QY 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSVPLDGGSGWEVFDIWKLF 300  
 DB 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSVPLDGGSGWEVFDIWKLF 300  
 QY 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360  
 DB 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360  
 QY 361 RSGQDDKTVYEYLFSSORRRRAPLATROGKRPSKNLKARCSRKALHVNFKDGMDDWIIA 420  
 DB 361 RSGQDDKTVYEYLFSSORRRRAPLATROGKRPSKNLKARCSRKALHVNFKDGMDDWIIA 420  
 QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPCCVPTRLSPISILFID 480  
 DB 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPCCVPTRLSPISILFID 480  
 QY 481 SANVVYKQYEDMVVESCGR 501  
 DB 481 SANVVYKQYEDMVVESCGR 501

RESULT 4  
 W11900  
 ID W11900 standard; Protein; 501 AA.  
 AC W11900;  
 DT 28-OCT-1997 (first entry)  
 DE Human high mol. wt. protein MP52, a growth/differentiation factor.  
 KW Growth factor; differentiation; bone induction; osteoporosis; teeth;  
 KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;  
 KW wound healing; regeneration; skeletal disorder; fracture; dimer.  
 OS Homo sapiens.  
 PN WO9704095-A1.  
 PD 06-FEB-1997.  
 PR 24-JUL-1996; J02065.  
 PA (FARH) HOECHST JAPAN LTD.  
 PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;  
 DR WPI; 97-132636/12.  
 DR N-PSDB; T61412.  
 PT High molecular weight human MP52 growth or differentiation factor -  
 PT promotes bone induction, is useful for treatment and prevention of  
 PT bone disease  
 PS Claim 1; Page 12-16; 25pp; Japanese.  
 CC W11900 is a high mol. wt. form of a human growth/differentiation  
 CC factor MP52. MP52 promotes bone induction and is useful for plastic  
 CC reconstructive surgery, cosmetic facial treatment, bone transplantation  
 CC and tooth implantation. It is also useful for the treatment and  
 CC prevention of disorders of bone formation, bone, cartilage, joint tissue,  
 CC skin, mucous membranes, nails or teeth; for wound treatment and tissue  
 CC regeneration; and for the treatment of skeletal disorders and fractures.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRLPKLLTFLWYLAWLDEFTICVLGAPDLGQRPQGTGRLGAKAEKRPPLARNVFRP 60  
 DB 1 MRLPKLLTFLWYLAWLDEFTICVLGAPDLGQRPQGTGRLGAKAEKRPPLARNVFRP 60  
 QY 61 GHSYGGGATNANARAGGTGQTGGLTQPKKDEPKKLPKPGGPEPKPGHPQTRQATAR 120

DB 61 GHSYGGGATNANARAGGTGQTGGLTQPKKDEPKKLPKPGGPEPKPGHPQTRQATAR 120  
 QY 121 TVTPKGLPGKAPPKAGSVSSFLKKAREPGPREKPPPPITPHEYMLSYRTL 180  
 DB 121 TVTPKGLPGKAPPKAGSVSSFLKKAREPGPREKPPPPITPHEYMLSYRTL 180  
 QY 181 SDADKGGNSSVKLEAGLANITTSFIDKQDDRGVVRKQRYVFDISALEKDGLLGAELR 240  
 DB 181 SDADKGGNSSVKLEAGLANITTSFIDKQDDRGVVRKQRYVFDISALEKDGLLGAELR 240  
 QY 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSVPLDGGSGWEVFDIWKLF 300  
 DB 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSVPLDGGSGWEVFDIWKLF 300  
 QY 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360  
 DB 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360  
 QY 361 RSGQDDKTVYEYLFSSORRRRAPLATROGKRPSKNLKARCSRKALHVNFKDGMDDWIIA 420  
 DB 361 RSGQDDKTVYEYLFSSORRRRAPLATROGKRPSKNLKARCSRKALHVNFKDGMDDWIIA 420  
 QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPCCVPTRLSPISILFID 480  
 DB 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPCCVPTRLSPISILFID 480  
 QY 481 SANVVYKQYEDMVVESCGR 501  
 DB 481 SANVVYKQYEDMVVESCGR 501

RESULT 5  
 W19210  
 ID W19210 standard; Protein; 501 AA.  
 AC W19210;  
 DT 04-MAR-1998 (first entry)  
 DE Human TGF-beta protein MP52.  
 KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;  
 KW cartilage; bone inducing activity; inhibit; bone resorption.  
 OS Homo sapiens.  
 PN DE19548476-A1.  
 PD 26-JUN-1997.  
 PR 22-DEC-1995; 048476.  
 PR 22-DEC-1995; DE-048476.  
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
 PI Bechtold R, Hotten G, Paulista M, Pohl J, Hoetten G;  
 DR WPI; 97-333931/31.  
 DR N-PSDB; T69695.  
 PT Compound containing protein from TGF-beta superfamily - has bone  
 PT and/or cartilage inducing activity, useful in treatment of, e.g.  
 PT osteoporosis, bone damage, Paget's disease and osteoarthritis  
 PS Claim 3; Page 9; 10pp; German.  
 CC This sequence is the human transforming growth factor (TGF)-beta protein  
 CC designated MP52. MP52 can be used in a compound of formula (I):  
 CC A-X(1-20)-B(1-20) (I): A = protein, or fragment, of the TGF-beta  
 CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);  
 CC B = 1 or more substituent groups with an affinity to the extracellular  
 CC matrix, cellular components of bone and/or cartilage and/or to a  
 CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer  
 CC groups. The compound may be used to inhibit bone resorption, prevent or  
 CC treat bone or cartilage related disorders, including osteoporosis,  
 CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthritis and  
 CC to treat bone or cartilage damage caused by wounding or overloading.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRLPKLLTFLWYLAWLDEFTICVLGAPDLGQRPQGTGRLGAKAEKRPPLARNVFRP 60  
 DB 1 MRLPKLLTFLWYLAWLDEFTICVLGAPDLGQRPQGTGRLGAKAEKRPPLARNVFRP 60



Query Match 100.0%; Score 2673; DB 1: Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPLARNVFRP 60  
 |||||  
 DB 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPLARNVFRP 60

QY 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVRRGGPEPKPHPPQTRQATAR 120  
 |||||  
 DB 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVRRGGPEPKPHPPQTRQATAR 120

QY 121 TVTPKGQPLGGKAPPGKAGSVSSFLKKAREPGPPREPKEFRPPPTTPHEYMVLSLYRTL 180  
 |||||  
 DB 121 TVTPKGQPLGGKAPPGKAGSVSSFLKKAREPGPPREPKEFRPPPTTPHEYMVLSLYRTL 180

QY 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVDFISALEKDGLLGAELR 240  
 |||||  
 DB 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVDFISALEKDGLLGAELR 240

QY 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPLDGSWEVDFDIWKLF 300  
 |||||  
 DB 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPLDGSWEVDFDIWKLF 300

QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
 |||||  
 DB 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360

QY 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420  
 |||||  
 DB 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420

QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFID 480  
 |||||  
 DB 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFID 480

QY 481 SANNVYKQYEDMVVESCGR 501  
 |||||  
 DB 481 SANNVYKQYEDMVVESCGR 501

RESULT 8  
 W44868  
 ID W44868 standard; protein; 501 AA.  
 AC W44868;  
 DT 24-SEP-1998 (first entry)  
 DE TGF-beta superfamily subunit.  
 KW TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;  
 KW bone replacement; cartilage; bone; fracture.  
 OS Synthetic.  
 PN DE19647853-A1.  
 PD 20-MAY-1998.  
 PF 19-NOV-1996; 047853.  
 PR 19-NOV-1996; DE-047853.  
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
 PA (GERO-) GERONTOCARE.  
 PA GMBH BIOMATERIALS & MEDICAL.  
 PI Heide H, Pabst J, Paulista M, Pohl J;  
 DR WPI; 98-287890/26.  
 PT Bioactive implant material for bone replacement - comprising  
 PT osteogenic calcium phosphate matrix coated with protein  
 PS Claim 3; Page 8-10; 12pp; German.  
 CC The TGF-beta superfamily subunit can be used together with a calcium  
 CC phosphate matrix to produce a bioactive implant material for bone  
 CC replacement. The implant has cartilage and/or bone-forming activity and  
 CC can be used for local treatment of cartilage and/or bone diseases or  
 CC damage caused by trauma, surgery, degeneration or overloading. The  
 CC implant can also be used for the treatment of bone defects, e.g.  
 CC parodontosis or fractures and in cosmetic and plastic surgery for fixing  
 CC mobile bones.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1: Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPLARNVFRP 60  
 |||||  
 DB 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPLARNVFRP 60

QY 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVRRGGPEPKPHPPQTRQATAR 120  
 |||||  
 DB 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVRRGGPEPKPHPPQTRQATAR 120

QY 121 TVTPKGQPLGGKAPPGKAGSVSSFLKKAREPGPPREPKEFRPPPTTPHEYMVLSLYRTL 180  
 |||||  
 DB 121 TVTPKGQPLGGKAPPGKAGSVSSFLKKAREPGPPREPKEFRPPPTTPHEYMVLSLYRTL 180

QY 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVDFISALEKDGLLGAELR 240  
 |||||  
 DB 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVDFISALEKDGLLGAELR 240

QY 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPLDGSWEVDFDIWKLF 300  
 |||||  
 DB 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPLDGSWEVDFDIWKLF 300

QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
 |||||  
 DB 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360

QY 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420  
 |||||  
 DB 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420

QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFID 480  
 |||||  
 DB 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFID 480

QY 481 SANNVYKQYEDMVVESCGR 501  
 |||||  
 DB 481 SANNVYKQYEDMVVESCGR 501

RESULT 9  
 R95635  
 ID R95635 standard; protein; 501 AA.  
 AC R95635;  
 DT 25-OCT-1996 (first entry)  
 DE Cartilage-derived morphogenetic protein-1.  
 KW Human; cartilage-derived morphogenetic protein-1; CDMP-1;  
 KW articular cartilage; chondrogenic; vulnery; implantation;  
 KW chondromalacia; osteoarthritis; therapy; joint repair.  
 OS Homo sapiens.  
 FH Key  
 FH Location/Qualifiers  
 FT peptide 2..19  
 FT /note= "Signal peptide"  
 FT region 2..377  
 FT /note= "Pro-region"  
 FT modified\_site 189..191  
 FT /note= "N-glycosylation site"  
 FT cleavage\_site 378..381  
 FT /note= "Proteolytic processing site"  
 FT domain 382..501  
 FT /note= "Mature C-terminal domain"  
 FT peptide 388..400  
 FT /note= "Antigen (R95642) used to raise antibodies"  
 FT peptide 417..447  
 FT /note= "Highly conserved consensus motif (R95641)"  
 PN W09614335-A1.  
 PD 17-MAY-1996.  
 PF 07-NOV-1994; U12814.  
 PR 07-NOV-1994; WO-U12814.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI Chang SC, Luyten FP, Moos M;  
 DR WPI; 96-251714/25.

DR N-PSDB: T31501.  
PT New purified cartilage extracts and proteins - used to stimulate the  
PT development and repair of cartilage in vivo.  
PS Claim 1; Fig 1; 34pp; English.  
CC The sequence represents human articular cartilage-derived  
CC morphogenetic protein-1 (CDMP-1). The protein contains a putative  
CC transmembrane signal peptide, a pro-region, a typical proteolytic  
CC cleavage site, and a C-terminal domain containing 7 highly  
CC conserved Cys residues characteristic of the transforming growth  
CC factor-beta gene family. A single N-glycosylation site is located  
CC in the pro-region. A 13-amino-acid peptide (R95642) has been used  
CC to raise rabbit polyclonal antibodies for screening of tissues for  
CC CDMP-1 expression. A consensus highly conserved motif in CDMP  
CC proteins (R95641) is present in the C-terminal domain. CDMP-1 is  
CC present in a purified cartilage extract (claimed) which stimulates  
CC local cartilage formation and repair when combined with a matrix  
CC and implanted in a mammal. The protein may be used in therapy of  
CC e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or  
CC to repair cartilage after reconstructive surgery.  
SQ Sequence 501 AA;

Query Match 98.4%; Score 2630; DB 1; Length 501;  
Best Local Similarity 98.4%; Pred. No. 2.5e-188;  
Matches 493; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRLPKLLTLLWYLAWLDELFTICVLGAPDLGQRPQGRPLGAKAKERPLARNVFRP 60  
DB 1 MRLPKLLTLLWYLAWLDELFTICVLGAPDLGQRPQGRPLGAKAKERPLARNVFRP 60  
QY 61 GHSYGGGATNANARAKGTGTGGLTPKDEPKLPKPPGPGPEKPHPPQTRQATAR 120  
DB 61 GHSYGGGATNANARAKGTGTGGLTPKDEPKLPKPPGPGPEKPHPPQTRQATAR 120  
QY 121 TVTPKQLPGKAPKAGSVSPSSFLKKAKEPPPREPEPPPPITPHEYMLSLYRTL 180  
DB 121 TVTPKQLPGKAPKAGSVSPSSFLKKAKEPPPREPEPPPPITPHEYMLSLYRTL 180  
QY 181 SDADKGGNSVKLEAGLANTITFTDKGDDRGVPVVRKQRYVDFISALEKDLGLGAEUR 240  
DB 181 SDADKGGNSVKLEAGLANTITFTDKGDDRGVPVVRKQRYVDFISALEKDLGLGAEUR 240  
QY 241 ILRKPSDTAKPAAGGAAQLKSSCPGROPASILLDVRSVPLDGSWEVDFIWKLF 300  
DB 241 ILRKPSDTAKPAAGGAAQLKSSCPGROPASILLDVRSVPLDGSWEVDFIWKLF 300  
QY 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
DB 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
QY 361 RSQDDKTYEYLFSSORRRRAPLATROGKRPSKNLKAACSRKALHVNFKMGWDDWIIA 420  
DB 361 RSQDDKTYEYLFSSORRRRAPLATROGKRPSKNLKAACSRKALHVNFKMGWDDWIIA 420  
QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTILNMSMDPESTPTCCVTRLSPISILFD 480  
DB 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTILNMSMDPESTPTCCVTRLSPISILFD 480  
QY 481 SANNVYKQYEDMNVESGCR 501  
DB 481 SANNVYKQYEDMNVESGCR 501

RESULT 10  
ID R60022 standard; Protein: 495 AA.  
AC R60022.  
DT 15-MAR-1995 (first entry)  
DE Growth differentiation factor 5.  
KW GDF-5; growth differentiation factor 5; diagnostic; therapeutic;  
KW detection; treatment; cell proliferative disorders; uterus tissue;  
KW skeletal tissue; uterine acoplasm; endometriosis; reagent;  
KW suppression; transforming growth factor beta superfamily; TGF beta.

OS Mus musculus.  
FH Key Location/Qualifiers  
FT modified\_site 183  
FT /note= "potential glycosylation site"  
FT cleavage\_site 371..375  
FT /note= "putative tetrabasic proteolytic processing  
FT site"  
FT cleavage\_site 384..385  
FT /note= "putative tetrabasic proteolytic processing  
FT site"  
PN W09415949-A.  
PD 21-JUL-1994.  
PR 12-JAN-1994; U00657.  
PA (UJO ) UNIV JOHNS HOPKINS SCHOOL MED.  
PI Huynh T, Lee S;  
DR WPI: 94-249127/30.  
DR N-PSDB: 070010.  
PT New growth differentiation factor-5 - used to develop prods. for  
PT the detection or treatment of cell proliferative disorders of the  
PT uterus or skeletal tissue  
PS Claim 1; Fig 1; 79pp; English.  
CC R60022 shows the amino acid sequence of Growth differentiation  
CC factor 5, which is encoded by 070010. The GDF-5 sequence contains  
CC a core of hydrophobic amino acids near the N-terminus, suggestive  
CC of signal conserved secretion. The sequence contains all of the  
CC highly conserved residues present in other members of the  
CC cysteine residues with their characteristic spacing. The prods. of the  
CC invention can be used for detection of a cell proliferative disorder  
CC of the uterus or skeletal tissue which is associated with GDF-5  
CC expression. Antisense sequences of GDF-5 can be used to treat uterine  
CC neoplasm, endometriosis, or skeletal disorders (claimed). The prods.  
CC can also be used in eg. contraception, in vitro fertilisation or in  
CC preventing premature labour.  
SQ Sequence 495 AA;

Query Match 89.8%; Score 2400; DB 1; Length 495;  
Best Local Similarity 91.2%; Pred. No. 3.2e-171;  
Matches 457; Conservative 7; Mismatches 31; Indels 6; Gaps 2;

QY 1 MRLPKLLTLLWYLAWLDELFTICVLGAPDLGQRPQGRPLGAKAKERPLARNVFRP 60  
DB 1 MRLPKLLTLLWYLAWLDELFTICVLGAPDLGQRPQGRPLGAKAKERPLARNVFRP 60  
QY 61 GHSYGGGATNANARAKGTGTGGLTPKDEPKLPKPPGPGPEKPHPPQTRQATAR 120  
DB 61 GHSYGGGATNANARAKGTGTGGLTPKDEPKLPKPPGPGPEKPHPPQTRQATAR 120  
QY 121 TVTPKQLPGKAPKAGSVSPSSFLKKAKEPPPREPEPPPPITPHEYMLSLYRTL 180  
DB 121 TVTPKQLPGKAPKAGSVSPSSFLKKAKEPPPREPEPPPPITPHEYMLSLYRTL 180  
QY 181 SDADKGGNSVKLEAGLANTITFTDKGDDRGVPVVRKQRYVDFISALEKDLGLGAEUR 240  
DB 181 SDADKGGNSVKLEAGLANTITFTDKGDDRGVPVVRKQRYVDFISALEKDLGLGAEUR 240  
QY 241 ILRKPSDTAKPAAGGAAQLKSSCPGROPASILLDVRSVPLDGSWEVDFIWKLF 300  
DB 241 ILRKPSDTAKPAAGGAAQLKSSCPGROPASILLDVRSVPLDGSWEVDFIWKLF 300  
QY 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
DB 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
QY 361 RSQDDKTYEYLFSSORRRRAPLATROGKRPSKNLKAACSRKALHVNFKMGWDDWIIA 420  
DB 361 RSQDDKTYEYLFSSORRRRAPLATROGKRPSKNLKAACSRKALHVNFKMGWDDWIIA 420  
QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTILNMSMDPESTPTCCVTRLSPISILFD 480  
DB 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTILNMSMDPESTPTCCVTRLSPISILFD 480

QY 481 SANNVYKQYEDMVVSCGCR 501  
Db 475 SANNVYKQYEDMVVSCGCR 495

RESULT 11  
R40800

ID R40800 standard; Protein; 401 AA.  
AC R40800; 11-FEB-1994 (first entry)  
DE TGF-beta-like clone MP-52 protein.  
KW Human; transforming growth factor; beta; TGF-beta; pharmaceutical;  
KW bone; cartilage; tooth; wound repair; immunosuppressor;  
KW organ transplant; cosmetic surgery; antibody; diagnosis.  
OS Homo sapiens.  
PN W09316099-A.  
PD 19-AUG-1993.  
PF 12-FEB-1993; E00350.  
PR 12-FEB-1992; EP-102324.  
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
PI Hoettgen G. Neidhardt H;  
DR WFI; 93-272824/34.  
DR N-PSDB; Q47709.  
PT New transforming growth factor-beta family proteins and DNA -  
PT used in tissue and wound repair, in treatment of bone, cartilage  
PT and tooth defects, and antibodies for diagnosis  
PS Claim 11; Page 19; 29pp; English.  
CC The sequences given in R40800 and R45447 represent fragments of embryo  
CC and liver derived human transforming growth factor-beta (TGF-beta)  
CC respectively. The full length protein may be used in a pharmaceutical  
CC composition for the treatment of various bone, cartilage or tooth  
CC defects and in tissue and wound repair processes. These proteins may  
CC also be used as immunosuppressors in organ transplants and in cosmetic  
CC surgery. Antibodies raised against these proteins may be used for  
CC diagnostic purposes.  
SQ Sequence 401 AA;

Query Match 79.98; Score 2133; DB 1; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.9e-151;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 PGGPEPKGHPQTRQATARTVTPKGOLPGKAPPKAGSVPSFLKKAREPGPPREPKE 160  
Db 1 PGGPEPKGHPQTRQATARTVTPKGOLPGKAPPKAGSVPSFLKKAREPGPPREPKE 60

QY 161 PFRPPPTPHEYMLSYRTLSADRKGNSSVKLEAGLANTITSFIDKGDDRGPPVVRKQ 220  
Db 61 PFRPPPTPHEYMLSYRTLSADRKGNSSVKLEAGLANTITSFIDKGDDRGPPVVRKQ 120

QY 221 RYVFDISALEKDGLLGALRIKRPKSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDV 280  
Db 121 RYVFDISALEKDGLLGALRIKRPKSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDV 180

QY 281 RSVPLDGSQWGVFDIWKLFERNFNKNSAQLCLELAWERGRAVDLRLGFGDRAARQVHEKA 340  
Db 181 RSVPLDGSQWGVFDIWKLFERNFNKNSAQLCLELAWERGRAVDLRLGFGDRAARQVHEKA 240

QY 341 LFLVFGRTKRRDLFFNFKARSQDDKTVVEYLFQSRKRRAPLATROGRKPSKNLKARC 400  
Db 241 LFLVFGRTKRRDLFFNFKARSQDDKTVVEYLFQSRKRRAPLATROGRKPSKNLKARC 300

QY 401 SRKALHNFXDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPES 460  
Db 301 SRKALHNFXDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPES 360

QY 461 TPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501  
Db 361 TPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 401

RESULT 12

R95636  
ID R95636 standard; Protein; 436 AA.  
AC R95636;  
DT 25-OCT-1996 (first entry)  
DE Cartilage-derived morphogenetic protein-2.  
KW Cattle; cartilage-derived morphogenetic protein-2; CDMP-2;  
KW articular cartilage; chondrogenic; vulnery; implantation;  
KW chondromalacia; osteoarthritis; therapy; joint repair.  
OS Bos taurus.  
FH Key  
FT region  
FT 1. .312  
FT /note= "Pro-region"  
FT modified\_site 89. .91  
FT /note= "N-glycosylation site"  
FT cleavage\_site 313. .316  
FT /note= "Proteolytic processing site"  
FT domain 317. .436  
FT /note= "C-terminal mature domain"  
FT peptide 352. .382  
FT /note= "Consensus conserved motif (R95641)"  
PN W09614335-A1.  
PD 17-MAY-1996.  
PF 07-NOV-1994; U12814.  
PR 07-NOV-1994; WO-U12814.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Chang SC, Luyten FP, Moos M;  
DR WFI; 96-251714/25.  
DR N-PSDB; T31602.  
PT New purified cartilage extracts and proteins - used to stimulate the  
PT development and repair of cartilage in vivo.  
PS Claim 11; Fig 2; 34pp; English.  
CC The sequence represents cattle articular cartilage-derived  
CC morphogenetic protein-2 (CDMP-2). The N-terminal methionine and  
CC signal peptide is missing, but part of the pro-region, a typical  
CC proteolytic cleavage site and a C-terminal domain containing 7  
CC highly conserved Cys residues characteristic of the transforming  
CC growth factor-beta gene family are present. A single N-glycosylation  
CC site is located in the pro-region. A consensus highly conserved  
CC motif in CDMP proteins (R95641) is present in the C-terminal domain.  
CC CDMP-2 is present in a purified cartilage extract (claimed) which  
CC stimulates local cartilage formation and repair when combined with a  
CC matrix and implanted in a mammal. The protein may be used in therapy  
CC of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or  
CC to repair cartilage after reconstructive surgery.  
SQ Sequence 436 AA;

Query Match 33.9%; Score 905.5; DB 1; Length 436;  
Best Local Similarity 42.5%; Pred. No. 5.1e-60;  
Matches 206; Conservative 65; Mismatches 109; Indels 105; Gaps 16;

QY 67 GGATNANAKGTTGGTGTGTPKDKPKLPKPPGPGPEPKGHPQTRQATARTVTPKG 126  
Db 7 GSAKGMRTKEGRMPRA-----PRENATAREPLDRQEPPEPQRR----- 51

QY 127 QLPGGKAPKAGSVPSFLKKAREPGPPREPKEPPPPPTPHEYMLSYRTLSADRK 186  
Db 51 -----PPQQ-----PEAREP-----PGRPLVPHEYMLSYRTSYIAEKL 86

QY 187 GGNSSVKLEAGLANTITSFIDKGDDRGPPVVRKQYVFDISAL-EKDGILGALRIK 244  
Db 87 GINASFQSKSANTITSFVDRGLDLSHTPLRRQYLFDFVSTLSKDELVDGLVRLFQ 146

QY 245 KPSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDVRSVPGLDGS---GWVFDIWKLF 301  
Db 147 APAALAPPAA---APLAALPLVAPAAGS-----AEPGPAGAPRPGWVFDVWRGLR 195

QY 302 NFKNASQLCLELE-AW--ERGRA-----VDRLGLGFDRAAQVHEKALFLV 344  
Db 196 P-QPWKQLCLELRAAWGEPGADEARTPGPOPPPPDLRLSLGFGRRVTPQERALLV 254

QY 345 FGRTKRRDLFFNFKAR-----SGDDKTVVEYLFQ 376  
Db 345 FGRTKRRDLFFNFKAR-----SGDDKTVVEYLFQ 376

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Db 255 FSRQKTL-FAEMREQLGSGATEVVGPGGAGSGPPPPPPSGTPDAGLWSP--SP 311
QY 377 RKRRAPLATROGKRPKNLKAARSRKALHVNFKMGWDWIIAIEAFCEGLCEFP 436
Db 312 GRRRTAFASRGRKGRKSRKSLKPLHVNFKELGWDWIIAIEAFCEGVCDFP 371
QY 437 LRSHLEPTNHAIVIQTLNMSMDPESTPTCCVTRLSPISILFIDSANNVYKQYEDMVVE 496
Db 372 LRSHLEPTNHAIVIQTLNMSMDPGSTPPSCCVTKLTPISILYIDAGNNVYNEYEMVVE 431
QY 497 SCGR 501
Db 432 SCGR 436

RESULT 13
ID R78730
AC R78730 standard; Protein; 321 AA.
DE 30-NOV-1995 (first entry)
KW Human mature VL-1 (BMP-13) encoding sequence.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..201
FT protein 202..321
FT misc_difference 202..321
FT misc_difference 220..321
FT /note="claimed"
FT /note="claimed"
FN W09516035-A.
PD 15-JUN-1995.
PR 06-DEC-1994; U14030.
PR 07-DEC-1993; US-164103.
PR 25-MAR-1994; US-217780.
PR 02-NOV-1994; US-333576.
PA (GENY) GENETICS INST INC.
PA (HARD) HARVARD COLLEGE.
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
PI WPI; 95-224320/29.
DR N-PSDB; Q96208.
PT Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
PT compsn. for inducing tendon/ligament-like tissue formation
PS Claim 14; Page 62-64; 84pp; English.
CC BMP-12 related proteins are a subset of the BMP/TGF-beta/Vg-1
CC family of proteins, including BMP-12 and VL-1. VL-1 is designated
CC BMP-13. Like BMP-12, it is expected that BMP-13, as expressed by
CC mammalian cells such as CHO cells, exists as a heterogeneous popn.
CC of active species of BMP-13 protein with varying N-termini. It is
CC expected that all active species will contain the AA sequence
CC beginning with the 19th Cys residue of the mature protein until
CC after the 120th residue of the mature protein or until the stop codon
CC species contain additional AA sequence in the N-terminal direction.
CC Q96208 is a partial DNA sequence and R78730 is the derived AA
CC sequence of a portion of the 2.5 kb DNA insert of the plasmid
CC subclone pGEMJLDC31/2.5, derived from clone lambdaJLDC31.
SQ Sequence 321 AA;

Query Match 28.8%; Score 771; DB 1; Length 321;
Best Local Similarity 51.1%; Pred. No. 3.7e-50;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 217 VRKQVVFYSAL-EKDGLLGALRLTRKPSDTAKPAAPGGGAAQL--KLSSCPGSRQ 273
Db 9 LRQKYLFDVMSLSKEELVGLRELFRQAPS-----APWGPPAGPLHVLFPCLS--- 60
QY 274 PASLLDVRSV--PGLDGGWEVFDIWKLFNFKNSAQLCLELE-AW---ERGRA----- 322
Db 60 -PLLLDARTLDPOGAPPAGWEVFDVWQGLRH-QPNKQLCLELRAAWGELDAGEARAG 117

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QY 322 -----VDLRGLGFDRARQVHKALFLVFGRTKKRDLFFNEIKARSGQDDKT----- 369
Db 118 PQQPPPDRLSLGFGRRVPPQERALLVVFTRSQKNL-FAEMREQLGSAEAGPGAGAE 176
QY 369 -----VYELFSQ-RRKRRAPLATROGKRPKNLKAARSRKALHVNFKMGWDW 416
Db 177 GSWPPPSGAPDARPLWLPSPGRRRRRTAFASRGRHGRKSLRCSKPLHVNFKELGWDW 236
QY 417 WIIAPLEYEAFHCEGLCEFPPLRSHLEPTNHAIVIQTLNMSMDPESTPTCCVTRLSPISI 476
Db 237 WIIAPLEYEAFHCEGVCDFPLRSHLEPTNHAIVIQTLNMSMDPGSTPPSCCVTKLTPISI 296
QY 477 LFIDSANNVYKQYEDMVVESCGR 501
Db 297 LYIDAGNNVYKQYEDMVVESCGR 321

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## RESULT 14

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ID W26591
AC W26591 standard; Protein; 321 AA.
DE 21-JAN-1998 (first entry)
KW Human bone morphogenetic protein BMP-13.
KW BMP-13; bone morphogenetic protein; human; tendon; ligament;
KW wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
KW therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..201
FT protein 202..321
FT /label= Sig_peptide
FT /label= Mat_protein
FT /note= "Claim 5"
FT /note= "Claim 5"
FN US565882-A.
PD 19-AUG-1997.
PR 07-DEC-1993; 164103.
PR 22-DEC-1994; US-362670.
PR 07-DEC-1993; US-164103.
PR 25-MAR-1994; US-217780.
PR 02-NOV-1994; US-333576.
PA (GENY) GENETICS INST INC.
PA (HARD) HARVARD COLLEGE.
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
PI WPI; 97-424270/39.
DR N-PSDB; T90386.
PT Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
PT - useful for tissue healing and repair, treatment of tendonitis,
PT improving fixation of tendons to bone etc
PS Claim 5; Column 57-60; 43pp; English.
CC This polypeptide comprises a novel bone morphogenetic protein. Its
CC amino acid sequence was deduced from isolated genomic clone vl-1
CC (see T90386). A claimed method for inducing formation of tendon
CC and/or ligament tissues involves the administration of a
CC composition containing at least one protein selected from BMP-13,
CC MP52 (see W26590) and BMP-12 (see W26589). The method is used for
CC tissue (including skin) healing and repair. This is useful for
CC treating tendonitis, carpal tunnel syndrome and other defects of
CC traumatic or congenital origin, in cosmetic surgery and to improve
CC fixation of tendons or ligaments to bone. The specified proteins
CC can also be used to increase activity of other BMPs e.g. BMP-2
CC (see W26597).
SQ Sequence 321 AA;

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Query Match 28.8%; Score 771; DB 1; Length 321;  
 Best Local Similarity 51.1%; Pred. No. 3.7e-50;  
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;





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Result No.	Score	Query Match	Length	DB	ID	Description
1	1433	53.6	324	13	Q9YHW9	Q9YHW9 gallus gall
2	989	37.0	257	13	Q42303	Q42303 brachydanio
3	844.5	31.6	412	13	O12938	O12938 brachydanio
4	567.5	21.2	126	13	Q93573	Q93573 gallus gall
5	455.5	17.0	400	13	O57574	O57574 brachydanio
6	444	16.6	361	5	O96504	O96504 brachiosteo
7	439.5	16.4	400	13	O13107	O13107 brachydanio
8	437	16.3	411	13	Q93369	Q93369 brachydanio
9	431	16.1	411	13	O57573	O57573 brachydanio
10	428.5	16.0	453	13	H87373	H87373 gallus gall
11	422	15.8	386	13	O13109	O13109 brachydanio
12	420	15.7	301	5	Q97390	Q97390 crassostrea
13	420	15.7	400	13	Q91703	Q91703 xenopus lae
14	419	15.7	390	13	Q91597	Q91597 xenopus lae
15	417	15.6	400	13	Q73818	Q73818 xenopus lae
16	412.5	15.4	391	13	H87380	H87380 brachydanio
17	409	15.3	411	13	O13108	O13108 brachydanio
18	405.5	15.2	614	5	P91720	P91720 drosophila
19	397	14.9	424	13	Q9YGH7	Q9YGH7 xenopus lae
20	391	14.6	373	13	O98950	O98950 gallus gall
21	390	14.6	421	11	Q921V8	Q921V8 mus musculus
22	385	14.4	373	13	Q90723	Q90723 gallus gall
23	382.5	14.3	354	13	Q9YGV1	Q9YGV1 xenopus lae
24	381.5	14.3	313	13	O91403	O91403 gallus gall
25	379.5	14.2	443	5	O76851	O76851 malocynthia
26	376.5	14.1	424	4	O95393	O95393 homo sapien
27	369.5	13.8	178	5	Q95211	Q95211 junonia coe
28	363	13.6	67	6	O02783	O02783 bos taurus
29	361.5	13.5	191	5	Q36468	Q36468 schistocerc

22. VNE KDMGMDWLT

22. VNE KDMGMDWLT

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QY 467 VPTRLSPISILFIDSANNVVKQYED 492
DB 299 VPTRLSPISILFIDSANNVVKQYEE 324

RESULT 2
O42303 PRELIMINARY: PRT: 257 AA.
AC O42303
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE CONTACT (FRAGMENT).
GN CONTACT.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RX MEDLINE: 97398455.
RA BRUNEAU S., MOURRAIN P., ROSA F.M.;
RT "Expression of contact, a new zebrafish DVR member, marks mesenchymal
RT cell lineages in the developing pectoral fins and head and is
RT regulated by retinoic acid."
RL Mech. Dev. 65:163-173(1997).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; Y12005; CAA72733.1;
DR PFAM; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR ZFIN; ZDB-GENE-990415-39; contact.
KW Glycoprotein.
FT NON_TER 1
FT CHAIN 140 257 POTENTIAL.
SQ SEQUENCE 257 AA; 29787 MW; 6BDDCADC CRC32;

Query Match 37.0%; Score 989; DB 13; Length 257;
Best Local Similarity 71.6%; Pred. No. 1.5e-75;
Matches 187; Conservative 25; Mismatches 45; Indels 4; Gaps 2;

QY 241 ILRKPSDTAKPAAGGAAOLKSSCPGROPASLLDVRSPVGLDGGWEVFDIWLK 300
DB 1 ILRKHMDSRKATFSEG--MAVRLFTCSAGNAVALLOARFDSHSASYEVFDIWKVF 58
QY 301 RNFKNSAQLCLEAWERGRAVLDRLGLFDRAARQVHEKALFLVFGRTKKRLDFFNEIKA 360
DB 59 KNFRNTPOLCLEDAVDHGRPLDLRLGLSRAGRTKEKAFVFWFGRTKKRLGLENEIKA 118
QY 361 RSGQDDKTYEYELFSORRRKRAPLATROGKRSKLNKARCSKALHVNFKMGWDDWIIA 420
DB 119 RSGHDKNTYELFTQRRMRAPLP--RGKKPKPKQRCNKRQLHVNFKMGWDDWIIA 176
QY 421 PLEYAFHCEGLCEPRLSHLEPHTHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480
DB 177 PLEYAFHCEGLCEPRLSHLEPHTHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 236
QY 481 SANNVVKQYEDMVVSCGCR 501
DB 237. SANNVVKQYEDMVVSCGCR 257

RESULT 3
O12938 PRELIMINARY: PRT: 412 AA.
AC O12938
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE DYNAMO PROTEIN PRECURSOR.
GN DYNAMO.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

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OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RX MEDLINE: 97398455.
RA BRUNEAU S., ROSA F.;
RT "Dynamo, a new zebrafish DVR member of the TGF-beta superfamily is
RT expressed in the posterior neural tube and is up-regulated by Sonic
RT hedgehog."
RL Mech. Dev. 65:199-212(1997).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; X99769; CAA68102.1;
DR PFAM; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR ZFIN; ZDB-GENE-980526-442; dynamo.
KW Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 293 412 DYNAMO PROTEIN.
SQ SEQUENCE 412 AA; 47071 MW; 1B5AEEL3 CRC32;

Query Match 31.6%; Score 844.5; DB 13; Length 412;
Best Local Similarity 50.0%; Pred. No. 3.7e-63;
Matches 179; Conservative 56; Mismatches 82; Indels 41; Gaps 12;

QY 167 ITPHEYMILSYLTSDADRGKSGNSKLEAGLANTITSFIDKQDD--RGPVVRKQRYVF 224
DB 73 IEPHYMISIVKTFSAEKLGLNASFFRSKANTITSFVDEGQDDHLSNPLWR-QKYL 131
QY 225 DISAL-EKDGLLGAELRLRK-KPSDTAKPAAGGAAOLKSSCPGROPASLLDVR 282
DB 132 DVSTLSENVEILGAELRIYTKISGFRASSETGP-----VEIQLLSC---QSHTVLD 182
QY 283 VPGLDG--SGWEVFDIWLKFR--NFKNSAQLCLEAW--ERGRAVLDRLGLGFPDRAARQ 335
DB 183 LDLEDAHPKWEVDFVWEIFKQRHSHGNRFLCUELRATLDPNPERIDQLYGLFHRHRP 242
QY 336 VHEKALFLVFGRTKKRLDFFNEIKARS---GQD-----DKTVYEYELFSORRRKRAP 383
DB 243 QLKRAILVFTRSKQSLFYEKREKIKLWGLDSTGKRRSHSKT-----RSRRTA 294
QY 384 LATROGKRSKLNKARCSKALHVNFKMGWDDWIIAFLYEAFHCEGLCEPRLSHLEP 443
DB 295 LPNRHGKRGHKKSRCSKPLHVNFKRELGLWDWVIAPLDYEAHCEGMDPFLRSHLEP 354
QY 444 TNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 501
DB 355 TNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 412

RESULT 4
O93573 PRELIMINARY: PRT: 126 AA.
AC O93573
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN GDF6/7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.
RN [1]
RX MEDLINE: 97398455.
RA LEE K.J., MENDELSON M., JESSELL T.M.;
RT "Neuronal patterning by BMPs: A requirement for GDF7 in the
RT generation of a discrete class of commissural interneurons in the
RT mouse spinal cord."
RL Genes Dev. 0:0-0(1998).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DB EMBL; AF089086; AAC97113.1;

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[illegible]

RESULT	6
O96504	
ID	PRELIMINARY; PRT; 361 AA.
AC	O96504;
DT	01-MAY-1999 (Tremblrel. 10, Created)
DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT	01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE	BONE MORPHOGENETIC PROTEIN 2/4.
GN	AMPHIBMP2/4.
OS	Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
CC	Branchiostoma.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE: 98401944.
RA	PANOPULOUI G.D., CLARK M.D., HOLLAND L.Z., LEHRACH H., HOLLAND N.D.;
RT	"AmphibMP2/4, an amphioxus bone morphogenetic protein closely related
RT	to Drosophila decapentagenic and vertebrate BMP2 and BMP4: Insights
RT	into evolution of dorsoventral axis specification.";
RL	Dev. Dyn. 213:130-139(1998).
CC	-I- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR	EMBL: AF068750; AAC97488.1;
DR	PROSITE; PS00250; TGF_BETA; 1.
KW	Glycoprotein.
SQ	SEQUENCE 361 AA; 41517 MW; 3C5F7E2S CRC32;
Query Match	16.6%; Score 444; DB 5; Length 361;
Best Local Similarity	33.0%; Pred. No. 1.3e-29;
Matches 126; Conservative	57; Mismatches 125; Indels 74; Gaps
Oy	155 PREPKEPRPPPIPTHYVMLSLRYTLSDARKGNGSSVKL-----EAGLANITTSFDIKG 2099
Dd	
Dd	19 PRPKNLVIIP-----YMELY--LSQT-KDPENPSVNFNAGKSTSTANTVRSFHHEE 69
Oy	: :
Oy	210 QDRGPVVVK-----QRVFVDISALEKDGLL-GAELRIILRKKPSDPTAKPAAPGGGRAAQ 2622
Dd	: :
Dd	70 ESEAGQPWEGDDEIDRRLFNTSAVPSVELIKAELRRLFREQID--VDHVQYGDSTDHH 127
Oy	: :
Oy	263 KLSCSFGROPAS-----LLDVRSVPGLDCGSWEVDFDWKLFRNFKNQAQ-----L 309
Dd	: :
Dd	128 LYRVNVIEVMRPNSTRNTDITRLLDTKLV-DVRNSSWESFDVRSAYTVKKNSPERNYGL 18
Oy	: :
Oy	310 CLELEANERG-----RAVDLRGLGDFDRAARQVEKALFLVCGTRKKDLFFNEIK 359
Dd	: :
Dd	187 EVEVSPKRGALSNHVLNRSTDM-----DDHSWQ-HRRPLLLTYTDGCKSGSNSNRVA 240
Oy	: :
Oy	360 ARSGODDKTVYEYLFSORRKRRAPLATROGKRPSKNLKARC SRKALHNFKMDMGWDWI 41

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Db 241 SRQKR-----ANGRKQR-----RLKAMCRHSLYVDFSDVGNWDIV 279
QY 420 APLEYFAHCEGLCEPPLSHLEPTNHAVIQTLNMSMDPESTPTCCVPTSLPSILFI 479
Db 280 APGYQAYCHCECPPLADLHNSHAIQTLNMSVNPVLAIVKACCVPTDLSISMLYL 339
QY 480 DSANNVYKQYEDVMVESCGR 501
Db 340 NENDQVLKYNQDMVVEGCGR 361

RESULT 7
O13107 PRELIMINARY; PRT; 400 AA.
AC O13107
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE BMP4.
GN BMP4.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
[1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE; 98036031.
RA MARTINEZ-BARBERA J.P., TORRESSON H., DAROCHA S., KRAUSS S.;
RT "Cloning and expression of three members of the zebrafish Bmp family:
RT Bmp2a, Bmp2b and Bmp4."
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; U82231; AAC60285.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 400 AA; 45757 MW; B95AE8FE CRC32;
```

Query Match 16.4%; Score 439.5; DB 13; Length 400;  
Best Local Similarity 31.7%; Pred. No. 3.5e-29;  
Matches 120; Conservative 66; Mismatches 112; Indels 81; Gaps 18;

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QY 163 RPP-----ITPHEYMLSYRTLSADKCGNSVKLE-----AGLANITTSF-----IDK 208
Db 63 RPPSHSAVVP-QYLLDLYLQSGEELAEAGHVSFDYPERSTSRASIVRGPHHEHLEE 121
QY 209 GDDRGVVRKQRYVDFISALEKDGLLG-AELRLKPKSDT-AKPAAPGGGAAQLK-- 265
Db 122 LQSD-GSQETPLRFVFNLSISPEDELSTADVKRIYRQIDDAFSDPDQDGHGLHRINII 180
QY 265 --LSSCPGSPASLLDVRSVPLDGSQWVEFDI-----WKLFRNFKNSAOLCILEAW 316
Db 181 EVLKAPREGQLITQLDLRLVRP-NTSKWESFDVSPAVLRWT--OEKRSNHLGAVVQM 237
QY 317 ER-----GRAVDRLGLGFDRAARQVHE-----KALFLVGRTKKRLDFFNEIKARS 362
Db 238 KRNPKVQGRHA-----RVRSRVHPLNEEDWHDVRLPLVTFGHGDKSHPL----- 282
QY 363 GDDKTVYELFSQRRKRAPLATQGRKPSKALHYNEKDKMGWDDWIIAPL 422
Db 282 -----TRAKRSP--KQGRKRN-----CRHAIYVDFSDVGNWDIVAPP 322
QY 423 EYFAHCEGLCEPPLSHLEPTNHAVIQTLNMSMDPESTPTCCVPTSLPSILFIDS 482
Db 323 GYQAYCHCECPPLADLHNSHAIQTLNMSVNPVLAIVKACCVPTDLSISMLYDET 381
QY 483 NNVVYKQYEDVMVESCGR 501
Db 382 DRVLKYNQDMVVEGCGR 400
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RESULT 8
O93369 PRELIMINARY; PRT; 411 AA.
AC O93369;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2.
GN BMP2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
[1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE; 97231284.
RA NIKAI DO M., TADA M., SAKI T., UENO N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning."
RL Mech. Dev. 61:73-88(1997).
[2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE; 98072322.
RA KISHIMOTO Y., LEE K.H., ZON L., HAMMERSCHMIDT M., SCHULTE-MERKER S.;
RT "The molecular nature of zebrafish swirl: BMP2 function is essential
RT during early dorsoventral patterning."
RL Development 124:4457-4466(1997).
[3]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE; 98072322.
RA LEE K.H., MARDEN J.J., THOMPSON M.S., MACLENNAN H., KISHIMOTO Y.,
RA PRATT S.J., SCHULTE-MERKER S., HAMMERSCHMIDT M., JOHNSON S.L.,
RA POSTLETHWAITE J.H., BEIER D.C., ZON L.I.;
RT "Cloning and Genetic Mapping of Zebrafish BMP-2."
RL Dev. Genet. 23:0-0(1998).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF072456; AAC25595.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46873 MW; AF0342A5 CRC32;
```

Query Match 16.3%; Score 437; DB 13; Length 411;  
Best Local Similarity 30.7%; Pred. No. 5.9e-29;  
Matches 122; Conservative 59; Mismatches 122; Indels 94; Gaps 1;

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QY 150 REPQPPREPKEPFRPPPTTPHEYMLSYRTLSADK-----RKGNSSVKLEAGLANTI 202
Db 64 RKTPSKSAVVP-----QYMLDLYMHSENDPNIIRPRSTMTGKHVERAASRANTI 114
QY 203 TSFID-----KGODRGVVRKQRYVDFISALEKDGLL-GAELRLKPKSDTAK 251
Db 115 RSFHHEAFELALLSGK-----TTQFFNLTSTPGEELISAAELRIFR---DQVLG 164
QY 252 PAAPGGGAAQL-----KLSSCPGSPASLLDVRSVPLDGSQWVEFDIWLFRNFKNSA 307
Db 165 DASTSGFHRINIYEVFRPALAPKEPLRLDLRLVQD-SHTRWESFDVGSVAWARWES 223
QY 308 Q-----LCLEL-----EAWERGRAVDRLGLGFDRAAROVH-----EKALFLVFG 346
Db 224 QHNHGLLVLEVLHPKESVSEAESENRKRV-----RVSRSLHAEDESWAQARPLLVTY- 277
QY 347 RTKRDLFNEIKARSGODDKTVYELFSQRRKRAPLATQGRKPSK--NLKARCSKA 404
Db 277 -----SHDGGGTAV-----LHNSREKQA-----RQGRKPKKHORNCRRHA 315
QY 405 LHVNFKMGWDDWIIAPLEYFAHCEGLCEPPLSHLEPTNHAVIQTLNMSMDPESTPT 464
Db 316 LYVDFSDVGNWDIVAPPYHAFYCHGCEPPLDHLNHNHAIQTLNMSVNPVLAIVKACCVPTDLSISMLYDET 374
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RP SEQUENCE FROM N.A.
RX MEDLINE: 98036031.
RA MARTINEZ-BARBERRA J.P., TORESSON H., DAROCHA S., KRAUSS S.:
RT "Cloning and expression of three members of the zebrafish Bmp family:
RL Bmp2a, Bmp2b and Bmp4."
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: U82233; AAC60287.1; -.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 386 AA; 43374 MW; 6BA60D2F CRC32;

Query Match 15.8%; Score 422; DB 13; Length 386;
Best Local Similarity 32.3%; Pred. No. 9.8e-28;
Matches 120; Conservative 63; Mismatches 117; Indels 72; Gaps 18;

QY 163 RPPITP---HEYMLSLYRTLS-DADR-----KGNSSVKLEAGLANTITSF-IDK 208
DB 163 RPPITP---HEYMLSLYRTLS-DADR-----KGNSSVKLEAGLANTITSF-IDK 208
QY 209 GODD--RGVVRKQRYVFDISALEKDLL-GAELRLIRKKPSDTAKPAAPGGGAAQLKL 265
DB 209 GODD--RGVVRKQRYVFDISALEKDLL-GAELRLIRKKPSDTAKPAAPGGGAAQLKL 265
QY 110 STEDPSSSVRTQRLFNLTSPDELYTSADVRFREQIVSSLNNSAGFHRINVHEI 169
DB 110 STEDPSSSVRTQRLFNLTSPDELYTSADVRFREQIVSSLNNSAGFHRINVHEI 169
QY 266 SSCPSC--RQPAS-LDVRSPGLDGSWEVFDIWLFRNFKNSAQLCLELAWERGRAV 322
DB 266 SSCPSC--RQPAS-LDVRSPGLDGSWEVFDIWLFRNFKNSAQLCLELAWERGRAV 322
QY 170 IR-PSGLQEPITRLDLTLVQH-SLSKWESEFDVTPAVLKTDTGHP-----NHGILV 220
DB 170 IR-PSGLQEPITRLDLTLVQH-SLSKWESEFDVTPAVLKTDTGHP-----NHGILV 220
QY 323 DLRLGLGF-----RAARQVHE-----KALFLVGRTKKRDLEFNEIKARSGQDDKT 369
DB 323 DLRLGLGF-----RAARQVHE-----KALFLVGRTKKRDLEFNEIKARSGQDDKT 369
QY 221 EISHPDQSRKHVRSRSLHNNEDTWSQMRPLLVTVSHDGNVLHS----- 268
DB 221 EISHPDQSRKHVRSRSLHNNEDTWSQMRPLLVTVSHDGNVLHS----- 268
QY 370 YEYLFQSRKRRLAPLATRQKRPKSKNLKARCSKALHVNFKDMGDDWIIAPLEYEAFH 429
DB 370 YEYLFQSRKRRLAPLATRQKRPKSKNLKARCSKALHVNFKDMGDDWIIAPLEYEAFH 429
QY 268 -----REKRA-----RNNKQKXK-KANCRHSLYVDFSDGVNDWIVAPGTHAFYC 315
DB 268 -----REKRA-----RNNKQKXK-KANCRHSLYVDFSDGVNDWIVAPGTHAFYC 315
QY 430 EGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVYKQ 489
DB 430 EGLCEPPLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVYKQ 489
QY 316 QGECPEPLADHLNSTNAMVQTLVNSN-SNIPRACCVPTDLSVSLYLDEYVERVILKN 374
DB 316 QGECPEPLADHLNSTNAMVQTLVNSN-SNIPRACCVPTDLSVSLYLDEYVERVILKN 374
QY 490 YEDMVVESCGR 501
DB 490 YEDMVVESCGR 501
QY 375 YQDMVVEGCGCR 386
DB 375 YQDMVVEGCGCR 386

RESULT 12
O97390
ID O97390 PRELIMINARY; PRT: 301 AA.
AC O97390
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE MGDF PRECURSOR.
GN MGDF.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoidae;
OC Ostreidae; Crassostrea.
RN [1]
RP SEQUENCE FROM N.A.
RA Lelong C., Mathieu M., Favrel P.;
RT "Structure and expression of mgdf, a new member of the TGF-beta
superfamily in Crassostrea gigas (Mollusca Bivalvia).";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: AJ130967; CAA10268.1; -.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Signal; Glycoprotein.
FT SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 301 MGDF PRECURSOR.
SQ SEQUENCE 301 AA; 34723 MW; B3B3E804 CRC32;

Query Match 15.7%; Score 420; DB 5; Length 301;
Best Local Similarity 33.9%; Pred. No. 1.1e-27;
Matches 106; Conservative 44; Mismatches 107; Indels 56; Gaps 10;

QY 222 YVFDISALE-KDGLGAEIRILIRKKPSDTAKPAAPGGGAAQLKLSGSGRPAS---- 277
DB 222 YVFDISALE-KDGLGAEIRILIRKKPSDTAKPAAPGGGAAQLKLSGSGRPAS---- 277
QY 12 FYFNVSIPVEESLTGAELRLFDQNNET----NPGVNRKQFRHKIETHEVLQPETANSE 67
DB 12 FYFNVSIPVEESLTGAELRLFDQNNET----NPGVNRKQFRHKIETHEVLQPETANSE 67
QY 277 ----LLDVRSPGLDGSWEVFDIWLFRNFKNSAQLCLELAWERGRAVDLRLGLGF-- 331
DB 277 ----LLDVRSPGLDGSWEVFDIWLFRNFKNSAQLCLELAWERGRAVDLRLGLGF-- 331
QY 58 AITRLDVRHVGK-KNSWESFDIHPAVLKWKKNTL-----NHGLKRVVLSEFNK 117
DB 58 AITRLDVRHVGK-KNSWESFDIHPAVLKWKKNTL-----NHGLKRVVLSEFNK 117
QY 331 -----RAARQV-----HEKALELVF-----GRKKRDLFFNEIKARSGQDDKT 368
DB 331 -----RAARQV-----HEKALELVF-----GRKKRDLFFNEIKARSGQDDKT 368
QY 118 PSTDSVKHVRRLRDVESVEAWHERPLLVTTDDNRSRTRKATSDKKVKKKKRKNK- 177
DB 118 PSTDSVKHVRRLRDVESVEAWHERPLLVTTDDNRSRTRKATSDKKVKKKKRKNK- 177
QY 369 VYEYLFQSRKRRLAPLATRQKRPKSKNLKARCSKALHVNFKDMGDDWIIAPLEYEAFH 428
DB 369 VYEYLFQSRKRRLAPLATRQKRPKSKNLKARCSKALHVNFKDMGDDWIIAPLEYEAFH 428
QY 177 -----NKKRNRK--KNRKNKTKRKYNNQCRKELNVDFKAVGNDWIFAPPGYNAY 228
DB 177 -----NKKRNRK--KNRKNKTKRKYNNQCRKELNVDFKAVGNDWIFAPPGYNAY 228
QY 429 CEGLCFEPPLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVYK 488
DB 429 CEGLCFEPPLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVYK 488
QY 229 CDGSHWYFDHMTNNAIVQDLVNSIDPRAAPKPCCVPTLSLSLTYIDHGAVALVK 288
DB 229 CDGSHWYFDHMTNNAIVQDLVNSIDPRAAPKPCCVPTLSLSLTYIDHGAVALVK 288
QY 489 QYEDMVVESCGR 501
DB 489 QYEDMVVESCGR 501
QY 289 YQDMVVEGCGCR 301
DB 289 YQDMVVEGCGCR 301

RESULT 13
O91703
ID O91703 PRELIMINARY; PRT: 400 AA.
AC O91703
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PROTEIN 4.
GN BMP-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA SMITH J.C.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE: 93048819.
RA DALE L., HOWES G., PRICE B.M., SMITH J.C.;
RT "Bone morphogenetic protein 4: a ventralizing factor in early Xenopus
development."
RL Development 115:573-585(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA METZ A., KNOEHEL S., BUECHLER P., KOESTER M., KNOEHEL W.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: X64538; CAA45836.1; -.
DR EMBL: AJ005076; CAA06333.1; -.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 400 AA; 45778 MW; 74ED45E8 CRC32;

Query Match 15.7%; Score 420; DB 13; Length 400;
Best Local Similarity 31.3%; Pred. No. 1.5e-27;
Matches 116; Conservative 58; Mismatches 127; Indels 70; Gaps 15;

```



[illegible]

RESULT	15
O73818	
ID	O73818
AC	PRELIMINARY;
DT	073818;
DT	01-AUG-1998 (TrEMBLrel. 07, Created)
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT	01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE	BONE MORPHOGENETIC PROTEIN 4.

GN BAP-4..  
OS *Xenopus laevis* (African clawed frog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Amphibia;  
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Xenopodinae;  
OC *Xenopus*.  
RN [1]  
RN SEQUENCE FROM N.A.  
RP  
RP KIM J., CHEN H.-D., ROH D.-H., AULT K.T., XU R.-H., PARK M.-J.,  
RA KUNG H.-F.;  
RA  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
CC 1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.  
DR EMBL: AF058764; AAC61694.1; -  
DR PFAM: PF00019; TGF-beta; 1.  
DR PFAM: PF00688; TGFb\_propeptide; 1.  
DR PROSITE: PS00250; TGF\_BETA; 1.  
KW Glycoprotein.  
SQ SEQUENCE 400 AA: 45810 MW: 399C1624 CRC32:

Db 187 NG-----LWIN-----RLDTRLIHH-NVTQWESFDVSPAIMRWTFDKQI----- 2266

Qy	316	WERGAVDVRGSLGFDRAKROVHEKALFVFGTKTKKDLFFNLRKASQDDAIVISILFS	37
Db	226	-NHGLAEVTHLQTKTHQCKHVRI-----SRSLJQE-----DADWSQMRPLLIIT	270
Qy	376	QRRKRRAPLATROGKRPCKNLKAR-----CSRKALHNVTKMGWDWIIAPLEYAFHCE	430
Db	271	FSDGGRGHALTRRKSRPKQORPKKNKCHRRHSLLVYDFSDVGWNDWVAPPQYQAFYCH	330
Qy	431	GLCEFFPLRSHLEPTNHAVIOTLNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQY	490

Db 331 GDCPFPLADHLNSTNHAIQTLVNSVN-ASIPKACCVPTLSAISMLYLDYDKVVLKNY 389  
QY 491 EDMVVECCGR 501  
Db :|||||  
Db 390 QEMVVECCGR 400

Search completed: October 31, 1999, 07:37:34  
Job time: 1333 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 29, 1999, 10:19:18 ; Search time 11.66 seconds  
(without alignments)  
1214.615 Million cell updates/sec

Title: US-09-297-092-1  
Perfect score: 2673  
Sequence: 1 MRLPKLLTLLWTLAWLDLE.....ANNVYQYEDMVVSCGCR 501

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt\_37.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2630	98.4	501	1	GDF5_HUMAN
2	2400	89.8	495	1	GDF5_MOUSE
3	905.5	33.9	436	1	GDF6_BOVIN
4	573	21.4	125	1	GDF6_MOUSE
5	510	19.1	151	1	GDF7_MOUSE
6	448	16.8	398	1	BMPA_XENLA
7	443.5	16.6	394	1	BMPA_MOUSE
8	440.5	16.5	396	1	BMP2_HUMAN
9	440.5	16.5	393	1	BMP2_RAT
10	434	16.2	513	1	BMP6_HUMAN
11	433	16.2	396	1	BMP2_DAMDA
12	433	16.2	405	1	BMP4_CHICK
13	432	16.2	398	1	BMPB_XENLA
14	428.5	16.0	461	1	DVRL_STRPU
15	428	16.0	452	1	BMP5_MOUSE
16	427.5	16.0	510	1	BMP6_MOUSE
17	427	16.0	593	1	DECA_DROSI
18	426.5	16.0	588	1	DECA_DROME
19	423	15.8	408	1	BMP4_HUMAN
20	422	15.8	401	1	BMP4_XENLA
21	420.5	15.7	454	1	BMP5_HUMAN
22	419	15.7	408	1	BMP4_MOUSE
23	417	15.6	408	1	BMP4_RAT
24	414	15.5	402	1	BMP8_HUMAN
25	408	15.5	408	1	BMP4_DAMDA
26	406.5	15.2	353	1	BMP2_CHICK
27	403	15.1	399	1	BMP8_MOUSE
28	402.5	15.1	383	1	UNIV_STRPU
29	401	15.0	621	1	DECA_DROPS
30	397.5	14.9	431	1	BMP7_HUMAN
31	396	14.8	430	1	BMP7_MOUSE
32	381	14.3	426	1	BMP7_XENLA
33	381	14.3	372	1	DECA_TRICA
34	374.5	14.0	427	1	DSLI_CHICK
35	370	13.8	472	1	BMP3_HUMAN
36	367	13.7	360	1	DVRL_XENLA
37	360.5	13.5	436	1	60A_DROVI
38	358	13.4	355	1	DVRL_BRARE
39	355.5	13.3	468	1	BMP3_RAT
40	349.5	13.1	399	1	BMP8_MOUSE
41	347	13.0	207	1	BMP6_RAT
42	343.5	12.9	372	1	GDF1_HUMAN
43	341	12.8	455	1	60A_DROME

44 328 12.3 476 1 BM3B\_MOUSE P97737 mus musculu  
45 316.5 11.8 476 1 BM3B\_RAT P55108 rattus norv

## ALIGNMENTS

RESULT	1
GDF5_HUMAN	
ID	GDF5_HUMAN STANDARD; PRT: 501 AA.
AC	P43026;
DT	01-NOV-1995 (REL. 32, CREATED)
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE	GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5) (CARTILAGE-DERIVED
DE	MORPHOGENETIC PROTEIN 1) (CDMP-1).
GN	GDF5 OR CDMP1.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-PLACENTA;
RX	HOETTEN G., NEIDHARDT H., JACOBOWSKY B., POHL J.;
RT	"Cloning and expression of recombinant human growth/differentiation
RT	factor."
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 204:646-652(1994).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=ARTICULAR CARTILAGE;
RX	MEDLINE; 95050604.
RA	CHANG S., HOANG B., THOMAS J.T., VUKICEVIC S., LUYTEN F.P.,
RA	RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.;
RT	"Cartilage-derived morphogenetic proteins. New members of the
RT	transforming growth factor-beta superfamily predominantly expressed
RT	in long bones during human embryonic development."
RL	J. BIOL. CHEM. 269:28227-28234(1994).
CC	FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC	SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC	TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING
CC	HUMAN EMBRYONIC DEVELOPMENT.
CC	DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC
CC	CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF
CC	DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE
CC	RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE
CC	METACARPALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE
CC	PHALANGES ARE ALMOST SQUARE.
CC	SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	EMBL; X80915; G671525; -
CC	EMBL; U13660; G600732; -
DR	MIM; 601146; -
DR	MIM; 201250; -
DR	MIM; 200700; -
DR	PROSITE; PS00250; TGF_BETA; 1.
DR	PFAM; PF00019; TGF-beta; 1.
DR	PFAM; PF00688; TGF-beta; 1.
DR	HSP; P18075; 1BMP.
DR	SIGNAL; GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
FT	SIGNAL 1 ? POTENTIAL.
FT	PROPEP ? 381 POTENTIAL.
FT	CHAIN 382 501 GROWTH/DIFFERENTIATION FACTOR 5.
FT	DISULFID 400 466 BY SIMILARITY.
FT	DISULFID 429 498 BY SIMILARITY.



```
RESULT 3
ID GDF6_BOVIN STANDARD; PRT; 436 AA.
AC P5106;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (CARTILAGE-DERIVED
DE MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT).
GN GDF6 OR CDMP2.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ARTICULAR CARTILAGE;
RX MEDLINE; 95050604.
RA CHANG S., HOANG B., THOMAS J.T., VUKICEVIC S., LUYTEN F.P.,
RA RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.;
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed
RT in long bones during human embryonic development.";
RL J. BIOL. CHEM. 269:28227-28234(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; U13661; G632490;
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
KW GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
FT NON_TER 1 1
FT PROPEP <1 316 POTENTIAL.
FT CHAIN 317 436 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 335 401 BY SIMILARITY.
FT DISULFID 364 433 BY SIMILARITY.
FT DISULFID 368 435 BY SIMILARITY.
FT DISULFID 400 400 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 27 27 POTENTIAL.
FT CARBOHYD 89 89 POTENTIAL.
SQ SEQUENCE 436 AA; 47873 MW; 4CC83ABC CRC32;

Query Match 33.9%; Score 905.5; DB 1; Length 436;
Best Local Similarity 42.5%; Pred. No. 1.1e-45;
Matches 206; Conservative 65; Mismatches 109; Indels 105; Gaps 16;

Qy 67 GGATNANARAKGGTGQTGLTPQKKDEPKLPPRPGGPEPKPGHPQPTQATATVTPKG 126
Dy 7 GSAGMTRKEGRMPRA-----PRENATAREPLDRQEPQPPRQEPQRR----- 51

Qy 127 QLPGKAPPKAGSVPSFLKAKREPGRPPKEFPPTTPHEYMILSYRLTSLDADRK 186
Dy 51 -----PPQO-----PEAREP-----PGRGRLVPHEYMILSYRTYSIAEKL 86

Qy 187 GNSSVKLEAGLANTITSFDKGDDGRPV-VRKORVVEDISAL-EKDGLLGAELRLRK 244
Dy 87 GINASFFOSSKSANTITSFVDRGLDLSHTPLRRQKYLFDVSTLSDEELVGADVRFLRQ 146

Qy 245 KPSDTAKPAAPGGGAOLKSSCPGROPASLLDVRSPGLDGS---GWEVEFDIWKFLR 301
Dy 147 APAALAPPA---APLAALRLPVAPAAGS-----AEPGACAPRPGWEVDFVWRGLR 195
```

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QY 302 NFKNSAQLCLELE-AW--ERGRA-----VDLRGLGFDRAARQVHEKALFLV 344
Dy 196 P-OPWKQLCLELELRAAWGEGPGAEDARTPGQPPPPDLRLSLGFGRRVRTPOERALLVV 254
QY 345 FGRTKKRDLFFNEIKAR-----SGQDDKTVYIYLFQ 376
Dy 255 FRSQRKTL-FAEMREQLGSATEVVGPGGAEGSGPPPPPPSGTDPAGLWSP--SP 311
QY 377 RKRRAPLATROGKRSKNLKARCSRKALHVNFKMGWDWDWIAPLEYAFHCEGLCEFP 436
Dy 312 GRRRTAFASRHGKRKSKRLRSLKPLHVNFKELGWDWDWIAPLEYAFHCEGVCDP 371
QY 437 LRSHLEPTNHAVIOTLMSMDPESTPTCCVTRLSPIFLFDSANNVYVYQYEDMVE 496
Dy 372 LRSHLEPTNHAVIOTLMSMDPGSTPPSCVPTKLTPI SILYIDAGNNVYVYEEYVE 431
QY 497 SCGR 501
Dy 432 SCGR 436

RESULT 4
ID GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (FRAGMENT).
GN GDF6 OR GDF-6.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE; 94195427.
RA STORM E.E., HUYNH T.V., COPELAND N.G., JENKINS N.A., KINGSLEY D.M.,
RA LEE S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily.";
RL NATURE 368:639-643(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; U08338; G488464;
DR MGD; MGI:95689; GDF6
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR HSP; P18075; IBMP.
KW GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
FT NON_TER 1 1
FT PROPEP <1 5 POTENTIAL.
FT CHAIN 6 125 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 24 90 BY SIMILARITY.
FT DISULFID 53 122 BY SIMILARITY.
FT DISULFID 57 124 BY SIMILARITY.
FT DISULFID 89 89 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 125 AA; 14373 MW; AEE04314 CRC32;

Query Match 21.4%; Score 573; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 4.1e-27;
Matches 99; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
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QY 130 GKAPKAGSVPSFLKKAREPGPPREP-----KEPRPPPTTPHEYMLSLYRT-LSADR 185  
DB 37 GRSPQSQVQLNQFELRLLSMFLKRRTPGKNVIPP-----YMLDYLHLAQLAA 90  
QY 186 KGNSSVKLE-----AGLANTITSFDKQDGRGVVYRK---QRYVFDISALEKDGILL-GA 237  
DB 91 DEGTSAQFQEMERAAQRANTVRSFHHEESMEETIPESREKTIQRFENLSSIPNEELVISA 150  
QY 238 ELRLRKPS-----DTAKPAAPGGGAAQLKSCPSGRQP-ASLDV 280  
DB 151 ELRFQVOEPESDKLHRLNIDYVKKPAA-----AASRGVVRLLDT 196  
QY 281 RSVPGDGGSGWEDVWKLFRNKSAQLCLELEW-----ERGRAVDLRLGLGFDRAAR 334  
DB 197 RLVHH-NESKWSFDVTP-----AIAHIAHQPNHGFVEVNLNDN---K 239  
QY 335 OVHEKALFLVFGTKRDLF--FNETKARGQDDKTYEYLFSSQRRKRAPLATROGKRP 392  
DB 240 NVPKKHVRISRLTPKDNWQIRLLVTFSHDGK---GHALHKRQKQA---RHQK- 292  
QY 393 SKNLKARCSKALHVNFKMGWDWIAPLEYEAFHCEGLCEPLSHLEPTNHAIQTL 452  
DB 292 -KRLKSCRRHPLVDFSDGVNDWIVAPPYHAFYCHGCEPPLADHLNSTHAIQTL 350  
QY 453 MNSMDPESTPTCCVPTLSILFIDSANNVYKQYEDMVVESCGR 501  
DB 351 VNSVN-TNPKACCVTELSAISMLYLDENEKVKVLYNQDMVVEGCGCR 398  
RESULT 7  
ID BMP2\_MOUSE STANDARD; PRT; 394 AA.  
AC P21274;  
DT 01-MAY-1991 (REL. 18, CREATED)  
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).  
GN BMP2 OR BMP-2.  
OS MUS MUSCULUS (MUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94289485.  
RA FENG J.Q.; HARRIS M.A.; GHOSH-CHOUDHURY N.; FENG M.; MUNDY G.R.;  
RA HARRIS S.E.;  
RT "Structure and sequence of mouse bone morphogenetic protein-2 gene  
and BMP-4 genes."  
RT and BMP-4 genes."  
RL BIOCHIM. BIOPHYS. ACTA 1218:221-224(1994).  
RN [2]  
RP SEQUENCE OF 1-351 FROM N.A.  
RX MEDLINE; 90228966.  
RA DICKINSON M.E.; KOBRIN M.S.; SILAN C.M.; KINGSLEY D.M.; JUSTICE M.J.;  
RA MILLER D.A.; CECI J.D.; LOCK L.F.; LEE A.; BUCHBERG A.M.;  
RA STRACUSA L.D.; LYONS K.M.; DERYNCK R.; HOGAN B.L.M.; COPELAND N.G.;  
RA JENKINS N.A.;  
RT "Chromosomal localization of seven members of the murine TGF-beta  
superfamily suggests close linkage to several morphogenetic mutant  
loci."  
RL GENOMICS 6:505-520(1990).  
CC -I- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
CC -I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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DR EMBL; L25602; G409362; -  
DR PIR; A34201; A34201  
DR MGI; 881177; BMP2.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
DR PFAM; PF00019; TGF-beta; 1.  
DR PFAM; PF00686; TGFb\_propeptide; 1.  
DR HSP; P18075; 1BMP.  
KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.  
FT SIGNAL; 1 ?  
FT PROPEP 280  
FT CHAIN 281 394  
FT DISULFID 293 359  
FT DISULFID 324 391  
FT DISULFID 327 393  
FT DISULFID 358 358  
FT CARBOHYD 134 134  
FT CARBOHYD 162 162  
FT CARBOHYD 198 198  
FT CARBOHYD 336 336  
FT CONFLICT 110 110  
FT CONFLICT 113 114  
FT CONFLICT 271 271  
SQ SEQUENCE 394 AA; 44514 MW; B055A5A9 CRC32;  
Query Match 16.6%; Score 443.5; DB 1; Length 394;  
Best Local Similarity 32.8%; Pred. No. 3.7e-19;  
Matches 131; Conservative 48; Mismatches 118; Indels 103; Gaps 19;  
QY 142 SSFLKKAREPGPPREPPTTPHEYMLSLYRTLSADRGKGNSSV-----KLE- 196  
DB 58 SMFGLKQR-----PTPSKDVVVP-----YMLDIYR-----RHSGQGPAPPHRLER 100  
QY 196 -AGLANTITSF-----IDKGQDRGVVYKQRYVEDISALEKDGILL-GAELRLRKPSD 248  
DB 101 AASRANTVTFHQLEAVEELPEMSGKTAR--RFFENLSSVPSDEFLTSAELQIFREIQOE 158  
QY 249 T-----AKPAAPGGGAAQLKSCPSGRQPASILLDVRSVPLDGSQHEV 293  
DB 159 ALGNSFSFOHRIYIIRKPA-----AANLKF---PVTR-----LLDTRLV-NONTSQMES 204  
QY 294 FDIWKLFRNFKNSAQ-----LCLEAWERGRAVDLRLGLGFDRAARQVHE-----KAL 341  
DB 205 FDTFVAVRWHTTQGHNTNGFVVEVAHLEENPGVSRHV---RISRLHQDEHSQIRPL 261  
QY 342 FLVFGTRTKRDLFFNEIKARSGQDDKTYEYLFSSQRRKRAPLATROGKRPKSLKARCS 401  
DB 262 LVTFGHDGK-----GPHLHKRKRQAKHKQR-----KRLKSSCK 295  
QY 402 RKALHVNFKMGWDWIAPLEYEAFHCEGLCEPLSHLEPTNHAIQTLNNSMDPEST 461  
DB 296 RHPLYVDFSDGVNDWIVAPPYHAFYCHGCEPPLADHLNSTHAIQTLNNSYN-SKI 354  
QY 462 PPTCCVPTLSILFIDSANNVYKQYEDMVVESCGR 501  
DB 355 PRACCVTELSAISMLYLDENEKVKVLYNQDMVVEGCGCR 394  
RESULT 8  
ID BMP2\_HUMAN STANDARD; PRT; 396 AA.  
AC P12643;  
DT 01-OCT-1989 (REL. 12, CREATED)  
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).  
GN BMP2 OR BMP2A.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89072730.

SEQUENCE FROM N.A.  
TISSUE=BONE;  
FENG J.Q., CHEN D., FENG M., HARRIS M.A., MUNDY G.R., HARRIS S.E.;  
SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
CC -!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.  
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: Z25868; G397951; -  
CC DR PROSITE; P500250; TGF\_BETA; 1;  
CC DR PFAM; PF00019; TGF-beta; 1;  
CC DR PFAM; PF00588; TGFb proceptide; 1;

[illegible]





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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: AJ001817; E352086; -  
CC PROSITE; PS00250; TGF\_beta; 1.  
CC PFAM; PF00019; TGF\_beta; 1.  
CC HSP; PF00688; TGF\_beta-propeptide; 1.  
CC HSP; P18075; 1BMP.  
CC SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.  
CC FT SIGNAL 1 2  
CC FT PROPEP 282  
CC FT CHAIN 283 396  
CC FT DISULFID 296 361  
CC FT DISULFID 325 393  
CC FT DISULFID 329 395  
CC FT DISULFID 360 360  
CC FT CARBOHYD 135 135  
CC FT CARBOHYD 163 163  
CC FT CARBOHYD 164 164  
CC FT CARBOHYD 200 200  
CC FT CARBOHYD 338 338  
CC SEQUENCE 396 AA; 44646 MW; 8C56358B CRC32;

DR EMBL: AJ001817; E352086; -  
DR PROSITE; PS00250; TGF\_beta; 1.  
DR PFAM; PF00019; TGF\_beta; 1.  
DR HSP; PF00688; TGF\_beta-propeptide; 1.  
DR HSP; P18075; 1BMP.  
DR SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.  
DR FT SIGNAL 1 2  
DR FT PROPEP 282  
DR FT CHAIN 283 396  
DR FT DISULFID 296 361  
DR FT DISULFID 325 393  
DR FT DISULFID 329 395  
DR FT DISULFID 360 360  
DR FT CARBOHYD 135 135  
DR FT CARBOHYD 163 163  
DR FT CARBOHYD 164 164  
DR FT CARBOHYD 200 200  
DR FT CARBOHYD 338 338  
DR SEQUENCE 396 AA; 44646 MW; 8C56358B CRC32;

Query Match 16.2%; Score 433; DB 1; Length 396;  
Best Local Similarity 30.4%; Pred. No. 1.5e-18;  
Matches 128; Conservative 51; Mismatches 132; Indels 110; Gaps 16;

QY 129 PGKAPKAGSVSSLLKARPGPPREPKEPPPTTPHEYMILSLRTLS-DADRKG 187  
DB 38 PGSSSQPSDDVLSEFELRLLSMFLGKQRP-TESRDPVVP--YMLDLYRLHSGQPGAPA 94  
QY 188 GNSSVKLEAGLANTITSF-----IDKGDDRGPPVWRKQRYVEDISAL-EKDGGLGAELEI 241  
DB 95 PGRHLERAASLANVTRTFHEESLEELPEMSGKTR--REFFNLTISPTFEFTISAELOV 152  
QY 242 LRKKPSDT-----AKPAPEGGRGAAQLKSSCPSPASLLDVRSPG 285  
DB 153 FGKHPPEALENNSFFHRIIFIRPATAN-----SKFPVTR---LLDTRLVT- 199  
QY 286 LDGSGWEVDIWLFRNFKNSAQLCLELEAWERGRAVDLRGLGF----- 330  
DB 199 ONASRWESFDV-----TPAVMRTAQGLTNHGTVVEVAHPEDSYGASKR 242  
QY 330 -DRAARQVHE-----KALFLVFGRTKKRDLFFNEIKARSGDDKTVVEYLFSSORRKR 380  
DB 243 HVRISRLHQDEHSWQIRPLLVTFGHGDK-----GHPHLHRRKR 282  
QY 381 RAPLATROGRKPKSKNKLARSKRKAHVNFKMGWDWIIAPLEYAFHCEGLCEFFLRSH 440  
DB 283 QAKHKOR-----KRLKSSCKRPLVYVDFSDGVNDWIVAPPYHAFYCHGCEPPLADH 336  
QY 441 LEPTNHAIVOTLNSMDPESTPTCCVPTPLSLPISILFIDSANNVYKQYEDWVVECCG 500  
DB 337 LNSTNHAIVOTLVNSVN-SKIPKACCVPTPLSLPISILFIDSANNVYKQYEDWVVECCG 395  
QY 501 R 501  
DB 396 R 396

RESULT 12  
ID BMP4\_CHICK  
BMP4\_CHICK STANDARD; PRT; 405 AA.  
AC Q90752;  
DT 01-NOV-1997 (REL. 35, CREATED)  
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).

GN BMP4 OR BMP-4.  
OS GALLUS GALLUS (CHICKEN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;  
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WHITE LEGHORN;  
RX MEDLINE; 94163974.  
RA FRANCIS P.H., RICHARDSON M.K., BRICKELL P.M., TICKLE C.;  
RT "Bone morphogenetic proteins and a signalling pathway that controls  
RT patterning in the developing chick limb";  
RL DEVELOPMENT 120:209-218(1994)  
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X75915; G472930; -  
CC PROSITE; PS00250; TGF\_beta; 1.  
CC PFAM; PF00019; TGF\_beta; 1.  
CC PFAM; PF00688; TGF\_beta-propeptide; 1.  
CC HSP; P18075; 1BMP.  
CC SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.  
CC FT SIGNAL 1 19  
CC FT PROPEP 20 291  
CC FT CHAIN 292 405  
CC FT DISULFID 305 370  
CC FT DISULFID 334 402  
CC FT DISULFID 338 404  
CC FT DISULFID 369 369  
CC FT CARBOHYD 144 144  
CC FT CARBOHYD 208 208  
CC FT CARBOHYD 347 347  
CC FT CARBOHYD 362 362  
CC SEQUENCE 405 AA; 46057 MW; A60C5A50 CRC32;

Query Match 16.2%; Score 433; DB 1; Length 405;  
Best Local Similarity 30.4%; Pred. No. 1.5e-18;  
Matches 123; Conservative 64; Mismatches 153; Indels 64; Gaps 14;

QY 125 KGQLPGGRAPKAGSVPSF-----LLKKAREPGPPREPKEPPPTTPHEYMILSLR 178  
DB 39 QGQAGSGRNSAOSHLLRGFTTLLQMGFLRRRPPQPSKSAVIP-----SYMDDLYR 89  
QY 179 TLSDADRKGNSSVKLE-----AGLANTITSFIDKGDDRG--VWRKQRYVFDISALE 230  
DB 90 LOSGEEERSLQEISLQYSPERSASRANVRSFHEEHLESVPSEAPRIREFVNLSSVP 149  
QY 231 KGLLGA-ELRLRKPSDTAKPAAPGGGAAQLKSSCPGSRQA--SLLDVRSVGLD 287  
DB 150 DNEVISSEELRLYREQVEBPSSAAWERGFRINIYEVMPKPLSERSQAITRLDTRLVHH-N 208  
QY 288 GSGWEVFDIWLFRNFKNSAQ-----LCLELEAWERGRAVDLRGLGFDRARQVHE----- 339  
DB 209 VTRWETFDVSPAVIRWTKDQPNHGLVIEVTHLHQATHQGHKVRISRLPGHGGDWAQ 268  
QY 339 -KALFLVFGRTKKRDLFFNEIKARSGDDKTVVEYLFSSORRKRAPLATROGRKSKNKL 397  
DB 269 LRPLLVTFGHGDRGHAL-----TRRRRSP--KHCGR--KN-K 302  
QY 398 ARCSKALHVNFKMGWDWIIAPLEYAFHCEGLCEFFLRSHLEPTNHAIVOTLVNSMD 457  
DB 303 KNCRRHALYVDFSDGVNDWIVAPPYHAFYCHGDCPPLADHLNSTNHAIVOTLVNSVN 362  
QY 458 PESTPTCCVPTPLSLPISILFIDSANNVYKQYEDWVVECCGR 501

Db	210	DVTP-----	-----A	ITR	IA	H	K	Q	N	H	G	F	V	E	V	T	H	L	D	N	T	N	P	K	H	R	V	I	R	S	L	T	D	K	256																							
QY	346	G	T	T	K	R	D	L	F	F	N	E	K	A	R	G	O	D	D	T	T	V	E	Y	I	F	S	O	R	K	R	R	A	P	I	A	T	Q	R	K	P	S	K	N	L	K	A	R	S	K	A	L	405					
Db	257	G	H	W	P	-----	-----I	R	P	L	T	F	S	H	D	G	-----	-----G	H	A	L	H	K	K	O	K	H	O	A	-----	-----R	H	K	O	R	-----	-----K	R	L	K	S	C	R	R	H	P	L	303										
QY	406	H	N	F	K	D	M	G	W	D	D	I	I	A	P	L	E	Y	A	E	F	H	C	E	G	L	C	E	F	P	L	S	R	L	E	P	T	N	H	A	V	I	O	T	L	N	S	M	D	P	E	S	T	P	T	C	465	
Db	304	Y	V	D	F	S	D	V	G	N	D	N	I	A	P	P	G	H	A	E	F	H	C	E	G	L	C	E	F	P	L	A	D	H	L	N	S	T	N	H	A	I	O	T	L	N	S	V	N	-----	-----T	N	I	P	K	A	C	362

RESULT	13
BMPB_XENLA	
ID	BMPB_XENLA
AC	P30884;
DT	01-JUL-1993 (REL. 26, CREATEL)
DT	01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DT	01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE	BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
OS	XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA.
NC	MESOBATRACHIA; PIPOIDEA; PIPOIDAE; XENOPODINAE; XENOPUS.
RN	[1]
STANDARD;	
PRT:	398 AA.

RESULT 14

DVRL_STRPU	ID	DVRL_STRPU	STANDARD;	PRT;	461 AA.
AC	P48969;				
DT	01-FEB-1996	(REL. 33,	CREATED)		
DT	01-FEB-1996	(REL. 33,	LAST SEQUENCE UPDATE)		
DT	01-FEB-1996	(REL. 33,	LAST ANNOTATION UPDATE)		
DE	DVRL-1	PROTEIN HOMOLOG	PRECURSOR.		
GN	DVRL-				

OS STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).  
 OC EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;  
 OC EUECHINOIDEA; ECHINACEA; ECHINOIDA; STRONGYLOCENTROTIDAE;  
 OC STRONGYLOCENTROTUS.  
 [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA PONCE M.R., MICOL J.L., DAVIDSON E.H.;  
 RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).  
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY

-- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY --

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or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).

CC EMBL; 248313; G673497; -  
CC PROSITE; PS00250; TGF-BETA; 1.  
CC PFAM; PF00019; TGF-beta; 1.  
CC PFAM; PF00688; TGF-beta-propeptide; 1.  
CC HSP; P18075; 1BMP.  
CC GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN; SIGNAL.  
CC SIGNAL 1 30  
CC PROPEP 31 338  
CC CHAIN 339 461  
CC DISULFID 360 426  
CC DISULFID 389 458  
CC DISULFID 393 460  
CC DISULFID 425 425  
CC CARBOHYD 149 149  
CC CARBOHYD 402 402  
CC SEQUENCE 461 AA; 51881 MW; 57C7CBA0 CRC3;  
CC SQ

FT	DISULFID	393		BY SIMILARITY.		
FT	DIFULFID	435		INTERCHAIN (BY SIMILARITY).		
FT	CARSOLD	149		POTENTIAL.		
FT	CARSOLD	149		POTENTIAL.		
FT	CARSOLD	402		POTENTIAL.		
SQ	SEQUENCE	461 AA:	51881 MW:	57C7CBA0 CRC32:		
	Query Match	16.0%;	Score	428.5;	DB 1:	Length 461;
	Best Local Similarity	29.7%;	Pred. No.	3.2e-18;		
	Matches 129;	Conservative	48;	Mismatches	105;	Indels 153;
						Gaps 17;

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SQ SEQUENCE 461 AA; 51891 MW; 57C7CBA0 CRC32;

Query Match 16.0%; Score 428.5; DB 1; Length 461;
Best Local Similarity 29.7%; Pred. NO. 3.2e-18;
Matches 129; Conservative 48; Mismatches 105; Indels 153; Gaps

QY 163 RPPPTTPHEVML-----SLYRTLSDDARKGGNSSVKLEAG----- 198
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 RPSLREGGQNCQAQFTWSYRYTLNIDQSGHPSETEPQPGCLASNAIYNSPDSGIGS 141

QY 198 -----LANITITS-----FDKGODRGPPVVKORYVEDISAL-EKQGL 234
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 VMSGTGVFNTRYRNEQVQSQADTMSLPVHYKDAIED-----TEHRYREDIGRIPOGETV 196

```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 1999, 07:02:15 : Search time 14.26 Seconds  
(without alignments)  
1407.630 Million cell updates/sec

Title: US-09-297-092-1  
Perfect score: 2673  
Sequence: 1 MRLPKLLTLLWYLAWLDE.....ANNVYKQYEDMVEVSCGCR 501

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database : PIR 60.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2673	100.0	501	JC2347	growth/differentia
2	2630	98.4	501	A53452	cartilage-derived
3	2400	89.8	495	A43294	bone morphogenetic
4	905.5	33.9	436	B53452	cartilage-derived
5	573	21.4	125	S43295	bone morphogenetic
6	510	19.1	151	S43296	bone morphogenetic
7	447	16.7	398	JH0688	bone morphogenetic
8	443.5	16.6	394	S45355	bone morphogenetic
9	440.5	16.5	396	BMH02	bone morphogenetic
10	440.5	16.5	393	S37073	bone morphogenetic
11	434	16.2	513	BMH06	bone morphogenetic
12	433	16.2	405	I50608	bone morphogenetic
13	432	16.2	398	JH0688	bone morphogenetic
14	428.5	16.0	461	S52408	bone morphogenetic
15	428	16.0	452	I49542	bone morphogenetic
16	427.5	16.0	510	A54798	Vg-1-related prote
17	426.5	16.0	588	A26158	decapentaplegic pr
18	423	15.8	408	BMH04	bone morphogenetic
19	422	15.8	401	JH0689	bone morphogenetic
20	420.5	15.7	454	BMH05	bone morphogenetic
21	420	15.7	400	A49147	bone morphogenetic
22	419	15.7	420	I49541	bone morphogenetic
23	417	15.6	408	S38343	bone morphogenetic
24	414	15.5	402	A45056	bone morphogenetic
25	409	15.3	408	JH0801	osteogenic protein
26	408	15.3	408	S58791	bone morphogenetic
27	406.5	15.2	353	I50607	bone morphogenetic
28	397.5	14.9	431	BMH07	bone morphogenetic
29	396	14.8	430	JQ1184	bone morphogenetic
30	381.5	14.3	313	I15284	bone morphogenetic
31	381	14.3	426	JH0690	bone morphogenetic
32	374.5	14.0	427	A40735	TGF beta homolog d
33	370	13.8	472	BMH03	bone morphogenetic
34	367	13.7	360	A29619	Vg1 embryonic grow
35	347	13.0	207	S37618	vgr protein - rat
36	343.5	12.9	372	C39364	GDF-1 embryonic gr
37	341	12.8	455	A43918	TGF-beta-related p
38	322	12.0	351	A34201	bone morphogenetic
39	316.5	11.8	476	JC4646	bone morphogenetic

growth/differentia  
bone morphogenetic  
bone morphogenetic  
bone morphogenetic  
transforming growt  
GDF-1 embryonic gr  
inhibin beta-A cha

ALIGNMENTS

RESULT 1  
JC2347  
growth/differentiation factor 5 - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Apr-1998  
C:Accession: JC2347  
R:Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.  
Biochem. Biophys. Res. Commun. 204, 646-652, 1994  
A:Title: Cloning and expression of recombinant human growth/differentiation factor-5.  
A:Reference number: JC2347  
A:Accession: JC2347  
A:Molecule type: DNA  
A:Residues: 1-501 <HOE>  
C:Genetics:  
A:Gene: GDB:BMH09  
A:Cross-references: GDB:433948  
A:Introns: 211/1  
C:Keywords: glycoprotein  
F:189/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 100.0%; Score 2673; DB 2; Length 501;  
Best Local Similarity 100.0%; Pred. No. 8e-172;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTLLWYLAWLDEFTCTVLGAPDLGCRPGTTPGLAKAEKRPPLARNVFRP 60  
DB 1 MRLPKLLTLLWYLAWLDEFTCTVLGAPDLGCRPGTTPGLAKAEKRPPLARNVFRP 60  
QY 61 GGHSGGGGATNANAKGGTGTGTGTPKDEPKKLPRPGGPPKPGHPPTQATAR 120  
DB 61 GGHSGGGGATNANAKGGTGTGTGTPKDEPKKLPRPGGPPKPGHPPTQATAR 120  
QY 121 TVTPKGQLPGGKAPKAGSVSPSSFLKKAREPGPREPKEPFPPIPTPHEYMLSLYRTL 180  
DB 121 TVTPKGQLPGGKAPKAGSVSPSSFLKKAREPGPREPKEPFPPIPTPHEYMLSLYRTL 180  
QY 181 SDADRRKGGNSVYKLEAGLANTITSTFDKGQDDRGPPVVRKQRYVFDISALEKDLGLGAEUR 240  
DB 181 SDADRRKGGNSVYKLEAGLANTITSTFDKGQDDRGPPVVRKQRYVFDISALEKDLGLGAEUR 240  
QY 241 ILRKPSDPTAKPAAPGGGAAAKLSSCPGSRQPASLLDVRSPVGLDGSWEVFDIWKLF 300  
DB 241 ILRKPSDPTAKPAAPGGGAAAKLSSCPGSRQPASLLDVRSPVGLDGSWEVFDIWKLF 300  
QY 301 RNFKNSAQCLCLEAWERGRAVDRLGRLGPDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
DB 301 RNFKNSAQCLCLEAWERGRAVDRLGRLGPDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
QY 361 RSGQDDKTYVYLFSSORRRRAPLATROGKRPSKLNKARCSKALHVNFKDGMWDWIIA 420  
DB 361 RSGQDDKTYVYLFSSORRRRAPLATROGKRPSKLNKARCSKALHVNFKDGMWDWIIA 420  
QY 421 PLEYEAFHCEGCEPFLRSHLEPTNHAVTQTLNMSMDPESTPTCCVPTRLSPISILFID 480  
DB 421 PLEYEAFHCEGCEPFLRSHLEPTNHAVTQTLNMSMDPESTPTCCVPTRLSPISILFID 480  
QY 481 SANNVYKQYEDMVEVSCGCR 501  
DB 481 SANNVYKQYEDMVEVSCGCR 501

```

RESULT 2
A55452
cartilage-derived morphogenetic protein 1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999
C:Accession: A55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth
A:Reference number: A55452; MUID:95050604
A:Accession: A55452
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-501 <CHA>
A:Cross-references: GB:U13660; NID:g600731; PID:g600732
C:Genetics:
A:Gene: GDB:CDMP1
A:Cross-references: GDB:438940

Query Match 98.4%; Score 2630; DB 2; Length 501;
Best Local Similarity 98.4%; Pred. No. 6e-169;
Matches 493; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MRLPKLLTFLWYLAWLDLEFICTVLGAPDLGQRPQGTTPGLAKAEKERPPPLARNVFP 60
Db 1 MRLPKLLTFLWYLAWLDLEFICTVLGAPDLGQRPQGTTPGLAKAEKERPPPLARNVFP 60
Qy 61 GGHSYGGGATNANARAKGGTGTGTLTKPKDEPKLPKPPGGPKPPHPPQTRQATAR 120
Db 61 GGHSYGGGATNANARAKGGTGTGTLTKPKDEPKLPKPPGGPKPPHPPQTRQATAR 120
Qy 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTTPHEYMLSLYRTL 180
Db 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTTPHEYMLSLYRTL 180
Qy 181 SDADKRGNSVVKLEAGLANITTSIDKGGDRGVPVVRKQRYVFDISALEKDGGLGAEIR 240
Db 181 SDADKRGNSVVKLEAGLANITTSIDKGGDRGVPVVRKQRYVFDISALEKDGGLGAEIR 240
Qy 181 SDADKRGNSVVKLEAGLANITTSIDKGGDRGVPVVRKQRYVFDISALEKDGGLGAEIR 240
Db 181 SDADKRGNSVVKLEAGLANITTSIDKGGDRGVPVVRKQRYVFDISALEKDGGLGAEIR 240
Qy 241 ILRKPSDTAKPAAPGGGAAQAQLKSSCPGROPASLLDVRSPGLDGSWEVDIWKLF 300
Db 241 ILRKPSDTAKPAAPGGGAAQAQLKSSCPGROPASLLDVRSPGLDGSWEVDIWKLF 300
Qy 241 ILRKPSDTAKPAAPGGGAAQAQLKSSCPGROPASLLDVRSPGLDGSWEVDIWKLF 300
Db 241 ILRKPSDTAKPAAPGGGAAQAQLKSSCPGROPASLLDVRSPGLDGSWEVDIWKLF 300
Qy 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
Qy 361 RSGQDDKTVYELFSORRRRAPLATROGKPSKLNKARCSKALHVNFKDMGWDWIIA 420
Db 361 RSGQDDKTVYELFSORRRRAPLATROGKPSKLNKARCSKALHVNFKDMGWDWIIA 420
Qy 421 PLEYEAFHCEGLCEPPLSHLEPTNHAIVQIOLMNSMDPESTPTCCVPTRLSPISILFID 480
Db 421 PLEYEAFHCEGLCEPPLSHLEPTNHAIVQIOLMNSMDPESTPTCCVPTRLSPISILFID 480
Qy 481 SANVVYKQYEDMVVESCGR 501
Db 481 SANVVYKQYEDMVVESCGR 501

RESULT 3
S43294
bone morphogenetic protein-related protein (GDF5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43294
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427
A:Accession: S43294

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <STO>

Query Match 89.8%; Score 2400; DB 2; Length 495;
Best Local Similarity 91.2%; Pred. No. 1.5e-153;
Matches 457; Conservative 7; Mismatches 31; Indels 6; Gaps 2;

Qy 1 MRLPKLLTFLWYLAWLDLEFICTVLGAPDLGQRPQGTTPGLAKAEKERPPPLARNVFP 60
Db 1 MRLPKLLTLLWLHLAWLDLELICTVLGAPDLGQRTPAKPGCLTKAEKERPPPLARNVFP 60
Qy 61 GGHSYGGGATNANARAKGGTGTGGLTQPKKDEPKLPKPPGGPKPPHPPQTRQATAR 120
Db 61 GGHIYGVGAT--NARAKGSSQ-----TQAKKDEPKPKPPRSGGSETPKPPSSQTRQAAAR 114
Qy 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTTPHEYMLSLYRTL 180
Db 115 TVTPKGQLPGGKASSKAGSAPSFLLKKTREPGTPREPKEPFPFPPTTPHEYMLSLYRTL 174
Qy 181 SDADKRGNSVVKLEAGLANITTSIDKGGDRGVPVVRKQRYVFDISALEKDGGLGAEIR 240
Db 175 SDADKRGNSVVKLEAGLANITTSIDKGGDRGVPVVRKQRYVFDISALEKDGGLGAEIR 234
Qy 241 ILRKPSDTAKPAAPGGGAAQAQLKSSCPGROPASLLDVRSPGLDGSWEVDIWKLF 300
Db 235 ILRKPKLDVAKPAVPSSGRVAQLKSSCPGROPAAALLDVRSPGLDGSWEVDIWKLF 294
Qy 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
Db 295 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 354
Qy 361 RSGQDDKTVYELFSORRRRAPLATROGKPSKLNKARCSKALHVNFKDMGWDWIIA 420
Db 355 RSGQDDKTVYELFSORRRRAPLATROGKPSKLNKARCSKALHVNFKDMGWDWIIA 414
Qy 421 PLEYEAFHCEGLCEPPLSHLEPTNHAIVQIOLMNSMDPESTPTCCVPTRLSPISILFID 480
Db 415 PLEYEAFHCEGLCEPPLSHLEPTNHAIVQIOLMNSMDPESTPTCCVPTRLSPISILFID 474
Qy 481 SANVVYKQYEDMVVESCGR 501
Db 475 SANVVYKQYEDMVVESCGR 495

RESULT 4
B55452
cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999
C:Accession: B55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Ko
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming gr
A:Reference number: A55452; MUID:95050604
A:Accession: B55452
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-436 <CHA>
A:Cross-references: GB:U13661; NID:g632489; PID:g632490

Query Match 33.9%; Score 905.5; DB 2; Length 436;
Best Local Similarity 42.5%; Pred. No. 1.2e-53;
Matches 206; Conservative 65; Mismatches 109; Indels 105; Gaps 16;

Qy 67 GGATNANARAKGGTGTGGLTQPKKDEPKLPKPPRGGPKPPHPPQTRQATARTVTPKG 126
Db 7 GSAKGMTRKEGRMPRA-----PRENATREPLDRQPPRPQPEPQR----- 51
Qy 127 QLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTTPHEYMLSLYRTLSDADRK 186

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QY 281 RSYVGLDGSWEVDIWKLFERNKNSAQICLLEAW-----ERGRAVDLRLGLGFDRAAR 334  
Db 197 RLVHH-NESKWSFDVTP-----AIARWIAHQPNHGVSFVTHLDND---K 239  
QY 335 QVHEKALFLVFGTKRDLF--FNEIKARSGODDKTVYELFSQRRKRAPLATROGRKP 392  
Db 240 NVPKKHVRISRLTPKDNWPIRLVTFSDGK---GHALHKRQKRA---RHQQR- 292  
QY 393 SNLKAARSRKALHVNFKDMGWDDWIIAPLEYAFHCEGLCFPPRLSHLEPTNHAVIQL 452  
Db 292 -KRLKSSCRHPLVDFSDVGNWDMIVAPPGYHAFYCHGCEFPPLADHLNSTHNAIVQL 350  
QY 453 MNSMDPESTPPCCVPTLSPISILFIDANNVYKQYEDMVVESCGR 501  
Db 351 VNSVN-TNIPKACCVPTLSAISMVLDENKVLKNYQDMVVEGCGR 398  
RESULT 8  
S45355  
bone morphogenetic protein-2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Dec-1994 #sequence\_revision 17-Nov-1995 #text\_change 03-May-1996  
C:Accession: S45355  
R:Feng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Mundy, G.R.; Harris, S.E.  
Biochim. Biophys. Acta 1218, 221-224, 1994  
A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comp  
A:Reference number: S45355; MUID:94289485  
A:Accession: S45355  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-394 <FEN>  
C:Superfamily: inhibin  
Query Match 16.6%; Score 443.5; DB 2; Length 394;  
Best Local Similarity 32.8%; Pred. No. 8.8e-23;  
Matches 131; Conservative 48; Mismatches 118; Indels 103; Gaps 19;  
QY 142 SFFLLKAREGPPRPKPFPPPTTPHEYMLSLYTLSDADRGKGNSSV-----KLE- 196  
Db 58 SMFGLKQR-----PTPSKDVVPP-----YMLDLYR-----RHSGQGPAPADHRLER 100  
QY 196 -AGLANTITSE-----IDKQDGRGPVVKQRYVFDISALEKDGLL-GAELRLKPKPSD 248  
Db 101 AASRAMTVIRFHEVAEPELPEMSGKTAR--RFFFLNLSVPDEFILTSAELOIFREQIOE 158  
QY 249 T-----AKPAAPGGGAAQLKLSGPCSGROPASLLDVRSPVGLDGSMEV 293  
Db 159 ALGNSFSQHRINIYEIKPA-----AANKLF---PVTR---LLDTRLV-NQNTSOWES 204  
QY 294 FDIWKLFERNKNSAQ-----LCLELEAWERGRAVDLRLGLGFDRAARQVHE-----KAL 341  
Db 205 FDTVPAMRWTTQGHTHNGFVVEVAHLEENPGVSKRHV---RISRLHODEHSWSQIRPL 261  
QY 342 FLVFGTKRDLFFNEIKARSGODDKTVYELFSQRRKRAPLATROGRKPKNKAARCS 401  
Db 262 LVTFGHDGK-----GHPLHKREKROAKHKQR-----KRLKSSCK 295  
QY 402 RKALHVNFKDMGWDDWIIAPLEYAFHCEGLCFPPRLSHLEPTNHAVIOTLMNSMDPEST 461  
Db 296 RHPLVDFSDVGNWDMIVAPPGYHAFYCHGCEFPPLADHLNSTHNAIVQLVNSVN-SKI 354  
QY 462 PPTCCVPTLSPISILFIDANNVYKQYEDMVVESCGR 501  
Db 355 PRACCVPTLSAISMVLDENKVLKNYQDMVVEGCGR 394  
RESULT 9  
BMH02  
bone morphogenetic protein 2 precursor - human  
N:Alternate names: bone morphogenetic protein 2A; rhBMP2  
C:Species: Homo sapiens (man)

C:Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 05-Sep-1997  
C:Accession: B37278; PC2178  
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.;  
Science 242, 1528-1534, 1988  
A:Title: Novel regulators of bone formation: molecular clones and activities.  
A:Reference number: A37278; MUID:89072730  
A:Accession: B37278  
A:Molecule type: mRNA  
A:Residues: 1-396 <WO2>  
A:Cross-references: GB:M22489; NID:gl79501; PID:gl79502  
R:Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Kat  
J. Biochem. 115, 279-285, 1994  
A:Title: Expression and characterization of human bone morphogenetic protein-2 in sil  
A:Reference number: PC2178  
A:Molecule type: protein  
A:Residues: 290-295, 'X', 297-304 <ISH>  
A:Experimental source: cell line BoMo-15ALIC  
R:Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J.  
Protein Sci. 4 (Suppl.2), 443S, 1995  
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (BMP-2  
A:Reference number: A56729  
A:Contents: annotation  
C:Note: determination of amino ends of mature forms: dimers with long form chains hav  
C:Comment: This hormone is capable of inducing bone formation at ectopic morphologica  
C:Genetics:  
A:Gene: GDB:BMP2; BMP2A  
A:Cross-references: GDB:125204; OMIM:112261  
A:Map position: 20p12-20p12  
C:Complex: homodimer, disulfide linked  
C:Superfamily: inhibin  
C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-265/Domain: propeptide #status predicted <PRO>  
F:266-396/Product: bone morphogenetic protein 2, long form #status predicted <MATL>  
F:283-396/Product: bone morphogenetic protein 2 #status predicted <MAT>  
F:135,163,164,200/Binding site: carboxylic acid (Gln) (in mature form) #status exper  
F:283/Modified site: pyrrolidone carboxylic acid (Asn) (covalent) #status exper  
F:338/Binding site: carboxylate (Asn) (covalent) #status experimental  
Query Match 16.5%; Score 440.5; DB 1; Length 396;  
Best Local Similarity 30.6%; Pred. No. 1.4e-22;  
Matches 136; Conservative 61; Mismatches 149; Indels 99; Gaps 19;  
QY 94 PKLLPFRPGPEPPHPOTROATRTVTKGQLPGGKAPPKAGSPVPSFLKKAREPG 153  
Db 14 PVLGLGGAAGLVPELG---RRKFAAASSGRFSSQ-----PSDEVLSFEFLRLSMFG 62  
QY 154 PPREKPEFRPPPTTPHEYMLSLYTLSDADRGKGNSSVLEAGLANTITSF-----ID 207  
Db 63 LKQRP-TPSRDAVVPP--YMLDLYRRHSGQSPAPDHLRLERAASRANTVRSFHHEESLE 119  
QY 208 KGODRGPVVKQRYVFDISAL-EKDGLLGAELRLTKPKPSDT-----A 250  
Db 120 ELPEFSGTKTR--RFFFLNLSIPTFEETISAELOVFEQMDALGNSSSFHHRINIYII 177  
QY 251 KPAAPGGGAAQLKLSGPCSGROPASLLDVRSPVGLDGSWEVDIWKLFERNKNSAQ-- 309  
Db 178 KPATAN-----SKFPVTR---LLDTRLV-NONASRWESFDVTPAVRW--TAQGH 221  
QY 309 ----LCLELEAWERGRAVDLRLGLGFDRAARQVHE-----KALFLVFGTKRDLFFN 356  
Db 222 ANHGFFVEVAHLEEKQGVSKRHV---RISRLHODEHSWSQIRPLLVTFGHDGK----- 273  
QY 357 EIKARSGODDKTVYELFSQRRKRAPLATROGRKPKNKAARCSRKALHVNFKDMGWDD 416  
Db 273 -----GHPLHKREKROAKHKQR-----KRLKSSCKRHPLVYDFSDVGNW 312  
QY 417 WIIAPLEYAFHCEGLCFPPRLSHLEPTNHAVIOTLMNSMDPESTPPTCCVPTLSPISI 476  
Db 313 WIVAPPGYHAFYCHGCEFPPLADHLNSTHNAIVQLVNSVN-SKIPKACCVPTLSAISM 371



QY 477 LFIDSANNVYKQYEDMVVESCGR 501  
 Db 372 LYLDENEKVLKYNQDMVVECCGR 396

RESULT 10

b37073  
 bone morphogenetic protein 2 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
 C:Accession: S37073  
 R:Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.  
 submitted to the EMBL Data Library, September 1993  
 A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein  
 A:Reference number: S37073  
 A:Accession: S37073  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <FEN>  
 A:Cross-references: EMBL:Z25868; NID:g397950; PID:g397951  
 C:Superfamily: inhibin

Query Match 16.5%; Score 440.5; DB 2; Length 393;  
 Best Local Similarity 31.7%; Pred. No. 1.4e-22;  
 Matches 133; Conservative 54; Mismatches 131; Indels 101; Gaps 19;

QY 137 AGVSPFLKAKREPGRPREKPF-----RPP-----TPHEYMISLY 177  
 Db 22 AGLPELGRKKFAGASRPSSEDLSEFELRLLSMFLGLKQPTPSKDVVPVPPMLDLY 81  
 QY 178 RTLSADARKGNSSV-----KLE--AGLANTISF-----IDKQDGRGVKQRYVFD 225  
 Db 82 R-----RHSGQPGALAPDRLEAARANTVLSFHHEAIEELSEMSTSR--REFN 133  
 QY 226 ISALEKDGLL--GAEIRILRKPSDTAKPAAPGGGAAQLKLS-----SCPSGORPAS- 277  
 Db 134 LSSVPTDEFLTSAELQIFRQMEAL-----GNSFQHRINIYELIKPATASKFPVTR 187  
 QY 277 LLDVRSVPGDGGSGWEVFDIWKLFNFKNSAQ-----LCELEAWERGRAVDLRGLGFD 330  
 Db 188 LLDRLVT-QNTSOWESFDTVPAMRW--TAQGHNTNHFVVEVAHLEKPKGSKRHV--- 242  
 QY 331 RAARQVHE-----KALFLVFGRTKKRLDFFNEIKARSGDDKTYVEYLFSSORRERA 382  
 Db 242 RISRLHODEHSWSQVRPLVTFGHGK-----GHLPHKREKROA 281  
 QY 383 PLATROGRKPSKNLKCRCRKALHVNFKMDGWDWIITAPLEYEAFHCEGLCEPPLRSHLE 442  
 Db 282 KHKQR-----KRLKSSCKRHPLVDFSDVGNWDWIIVAPGYHAFYCHGCPPLADHLN 335  
 QY 443 PTNHAIVQTLNMSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501  
 Db 336 STNHAIVQTLNVSNN-SKIPKACCCVPTLSAISMLYLDENEKVVYLNQDMVVECCGR 393

RESULT 11

b37068  
 bone morphogenetic protein 6 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 18-Oct-1991 #sequence\_revision 03-Aug-1995 #text\_change 18-Sep-1998  
 C:Accession: B39263  
 R:Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, P.; Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990  
 A:Title: Identification of transforming growth factor beta family members present in bone morphogenetic protein 6 precursor  
 A:Reference number: A39263; MUID:91088608  
 A:Accession: B39263  
 A:Molecule type: mRNA  
 A:Residues: 1-513 <CEL>  
 A:Cross-references: GB:M60315; GB:M38694; NID:g339561; PID:g339562  
 C:Genetics:  
 A:Gene: GDB:BMP6  
 A:Cross-references: GDB:127596; OMIM:112266

A:Map position: 6pter-6qter  
 C:Superfamily: inhibin  
 C:Keywords: bone; glycoprotein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-374/Domain: propeptide #status predicted <PRO>  
 F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>  
 F:241,269,386,404,454/Binding site: carbohydrate (Asn) #status predicted

Query Match 16.2%; Score 434; DB 1; Length 513;  
 Best Local Similarity 27.4%; Pred. No. 5.1e-22;  
 Matches 156; Conservative 69; Mismatches 197; Indels 148; Gaps 25;

QY 12 WYLAWLDELFICTVLCAPDLGQRPQTRPGLAKAEKERPPPL-ARNVFRPGHSYGGGAT 70  
 Db 10 WLCWMMGL--LCSCCGPPPL-----RPLPAAAAAAGGOLLGDS 49  
 QY 71 NANARAKGGTGTGG-----LTQPKDBPKPKLPKPGGP-EPKPGH-----PPOTRQ 116  
 Db 50 PGTEQPPSPQSSSGFLYRLKTKQEKREKQELSLVGLPHRPLHGLQOPPPALRQ 109  
 QY 117 ATARTVTPKGQPGKAPKAGVPSS--FLL-----KKAREPGPPRE- 158  
 Db 110 QEQ--OQQQLPRGPPP--GRKXGAPLFMLDLYNALSADNEDCAGEGEOQSWPHEA 165  
 QY 158 --PKFPRPPPTPHEYMISLYRTLSADARKGNS---SVKLEAGL--ANTTISFDKGO 210  
 Db 166 ASSQRRQPPPGAHP--LNRKSLAPGSGSGGASPLTSAQDSAFNLNDADVMVSYNLVE 223  
 QY 211 DDR--GPVYRKOR--YVFDISAL--EKDGLLGAELRLRKPKPSDTAKPAAPGGGAAQLKLS 266  
 Db 224 YKFEFPRHHKFEKFNLSQIPEGVVTAAEFRIY-----KDCVMGSKNQTFLLIS 275  
 QY 267 SCPSGRQ-----PASLLDVRSVPGDGGSGWEVFDI-----WKLFRNFKNSAQCLCLE 314  
 Db 276 IYQVLQEHQHRSDDLFLDTRVWASE--EGWLEFDTATSNLWVTPQHNMGLQLSV--- 332  
 QY 315 AWEGRGAVDLRGLGFPRAARQVHEKALFLVFGRTKKRDLEFNEIKARSGDDKTYVEYLF 374  
 Db 332 -----VTRDGVHVHPRAAGLV-----GRDGYDKQPFMVAE 362  
 QY 375 SQ-----RKRRAPLATRQGR-----PSKNLKCRCRKALHVNFK 410  
 Db 363 FKVSEVHVVTTSASSRRQQRNRSTQSDQVARVSSASDYNSELKTACRKHELIVSFQ 422  
 QY 411 DMGWDWIITAPLEYEAFHCEGLCEPPLRSHLEPTNHAIVQTLNMSMDPESTPTCCVPTR 470  
 Db 423 DLGQDWIITAPKYAANYCDGECSPFLNAHMNATNHAIVQTLNLMNPEVVPKPCCAPTK 482  
 QY 471 LSPISILFIDSANNVYKQYEDMVVESCGR 500  
 Db 483 LNAISVLYFDDNSNVILKKRYNNMVRACGC 512

RESULT 12

b37068  
 bone morphogenetic protein 4 - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 23-Feb-1997  
 C:Accession: I50608  
 R:Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.  
 Development 120, 209-218, 1994  
 A:Title: Bone morphogenetic proteins and a signalling pathway that controls pattern in the chick embryo  
 A:Reference number: I50607; MUID:94163974  
 A:Accession: I50608  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-405 <FRA>  
 A:Cross-references: EMBL:X75915; NID:g472929; PID:g472930  
 C:Genetics:  
 A:Gene: Bmp-4  
 C:Superfamily: inhibin

Query Match 16.2%; Score 433; DB 2; Length 405;  
Best Local Similarity 30.4%; Pred. No. 4.6e-22;  
Matches 123; Conservative 64; Mismatches 153; Indels 64; Gaps 14;  
QY 125 KOQLPGKAPKAGVPSFSF-----LLKAREPGPPREPPEPPPPITPHEYMLSLYR 178  
DB 39 QOAGSGRRSAQSHLLRGFETTLQMFGLRRPQPSKSAVIP-----SYMLDIYR 89  
QY 179 TLSDADRGKGNSSVKLE-----AGLANITTSFIDKGDDRGD---VVRKQYVFDSALE 230  
DB 90 LOSGEEERSLOEISLOXPERSASRANTVRSFPHHEHLESVPGPSEAPRIREFVNLSSVP 149  
QY 231 KDGLLGA-ELRLRKPSDTAKPAAPGGRAAQLKSCPSGRQPA--SLLDVRSVPGLD 287  
DB 150 DNEVSSBELRLYRQVEEPSAAMWGRFHRIYEVKMPKLSERSQAITRLDTRLVHH-N 208  
QY 288 GSGWVFEDIWLFNRFNKSAQ-----LCLEAWERGRAVDLRLGLGFDRAARQVHE----- 339  
DB 209 VTRWETEDVSPAVIRWTKDQPNHGLVIEVTHLQAQTHOGKHVIRISLSLPGHGGDWAQ 268  
QY 339 -KALFLVGRKTRKDLFEINEIKARGQDDKTVYELFSQRRKRRAPLATROGKPSKNLK 397  
DB 269 LRPLLVTEGHDGRHAL-----TRRARRSP--KHHGSR--KN-K 302  
QY 398 ARCSKALHVNFKMGWDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIOTLMSND 457  
DB 303 KNCRRHALYVDSVDGNDWIAPPGYQAFYCHGCPPLADHLNSTHAIIVOTLVNSVN 362  
QY 458 PESTPTCCVPTLSPISLIFDSANNVYKQYEDMWVSCGCR 501  
DB 363 -SSIPKACVPTLSAISMLYLDKVKVLYKNYQEMVVEGCGCR 405

RESULT 13  
JH0688  
bone morphogenetic protein 2II precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Sep-1997  
C:Accession: JH0688  
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.  
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992  
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a  
A:Reference number: JH0687; MUID:92378616  
A:Accession: JH0688  
A:Molecule type: mRNA  
A:Residues: 1-398 <NTS>  
A:Cross-references: GB:X63425; NID:g64583; PID:g64584  
A:Experimental source: oocyte  
C:Superfamily: inhibin  
C:Keywords: glycoprotein  
F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>  
F:137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 432; DB 2; Length 398;  
Best Local Similarity 32.1%; Pred. No. 5.3e-22;  
Matches 127; Conservative 62; Mismatches 143; Indels 64; Gaps 18;  
QY 133 APPKAGSVPSFLLKAREPGPPREP---KEPFRPPPTPHEYMLSLYRTLSD--ADRGK 187  
DB 40 SPQSQQVLDQFELLLNMFLKRRPTGKNVIPP-----YMLDLYLHLSAQLADDOG 93  
QY 188 GNS---SVKLEAGLANITTSIDKGDDRGVVRK---QRVVDISALEKGLL-GAELR 240  
DB 94 SSEVDYHMERASRANTVRSFPHHEESMEIEIPESGKTIQREFFNLSSIPDEBELVTSSEL 153  
QY 241 ILRKPSDTAKPAAPGGRAAQLK-----SSCPGSRGP-ASLLDVRVPGLDGSGVEVF 294  
DB 154 IFREQ---VQEPFKTDGSKLLHRIINIDYIVKPAASRGVVRLLDTRLIHH-NEKSWESF 209  
QY 295 DIWKLFRNFKNSAQLCLEAW-----ERGRAVDLRLGLGFDRAARQVH---EKALFLVF 345

Db 210 DVTP-----AITRWIAHKQPNHGCFVVEVTHLNDNTNPKRHVIRISRLTLDK 256  
QY 346 GRTKKRDLFFNEIKARGQDDKTVYELFSQRRKRRAPLATROGKPSKNLKARCSKAL 405  
DB 257 GHWPR---IRPLLVTFSDHGK---GHALKHQRKQA-----RHQR--KRLKSSCRRHPL 303  
QY 406 HVNFKMGWDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIOTLMSNDPESTPTTC 465  
DB 304 KYVDSDDGNDWIAPPGYHAFYCHGCEPPLADHLNSTHAIIVOTLVNSVN-TNPKAC 362  
QY 466 CVPTLSPISLIFDSANNVYKQYEDMWVSCGCR 501  
DB 363 CVPTLSAISMLYLDENEKVKVLYKNYQEMVVEGCGCR 398  
RESULT 14  
S52408  
SPDVRL protein - sea urchin (Strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Sep-1997  
C:Accession: S52408  
R:Ponce, M.R.; Micol, J.L.; Davidson, E.H.  
submitted to the EMBL Data Library, February 1995  
A:Description: SPDVRL, a member of the transforming growth factor-beta superfamily ex  
A:Reference number: S52408  
A:Accession: S52408  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <PON>  
A:Cross-references: EMBL:Z48313; NID:g673496; PID:g673497

Query Match 16.0%; Score 428.5; DB 2; Length 461;  
Best Local Similarity 29.7%; Pred. No. 1.1e-21;  
Matches 129; Conservative 48; Mismatches 105; Indels 153; Gaps 17;

QY 163 RPPPTITHEYML-----SLYRTLSADRKGNSSVKLEAG----- 198  
DB 82 RPPSLRGQNOFCAOFTWESYRTLNIDEQSGHPSETEPOPGGLASNAIYNPSDSSIGS 141  
QY 198 -----LANTITS---FTDKGQDDRGVVRKQRYVFDISAL-EKDGL 234  
DB 142 VMSGTVNYTRNEVQVQADTMSLPVHYKDAIED-----FEHRYRFDIGRIPQGETV 196  
QY 235 LGAEILRLRKPSDTAKPAAPGGRAAQLKSCPSGRQPAFL--LDVRSY--PGLDGS- 290  
DB 197 TSAELRVR-----DAGRQGRSLYRIDVLLRLRSGDSGR 231  
QY 290 -----GWEVEDI-----WKLFRNFKNSAQLCLEAWERGRAVDLRLGLG 328  
DB 232 SPVYLDSTIVGAGDHGLVDFDMSATSTWRSYPGANYGLQL-----RVESLQGLN 281  
QY 329 FDRAARQVHEKALFLVFGRTKKRD---LFFNEIKARGSGDDKTVYELFSQRRKRAPL 384  
DB 282 IDPTDAGV-----VGVGNNEGREFPMVVF-----ORNEEVIATNSHLRNRRA-- 326  
QY 385 ATRO---GKRPSK-----NLKARCSKALHVNFKMGWDWIIAPLEYE 425  
DB 326 ATROKGGKRPKRPDPTDNDIASRDSASSLSNDWQCKRKNLFVNFEDLDWOEWIAPLYV 385  
QY 426 AFHCEGLCEPPLSHLEPTNHAVIOTLMSNDPESTPTCCVPTLSPISLIFLDSANNV 485  
DB 386 AFYCGGCAFLNGHANATNHAIIVOTLVHMSHSPVQPCCAPTKLSPTIYLYDSSRN 445  
QY 486 VYKQYEDMWVSCGCR 500  
DB 446 VLKYYKNVVRACGC 460

RESULT 15  
I49542  
bone morphogenetic protein 5 - mouse  
C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Feb-1997

C:Accession: I49542

R:King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.

Dev. Biol. 166, 112-122, 1994

A:Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice

A:Reference number: I49542; MUID:95046894

A:Accession: I49542

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-452 <RES>

A:Cross-references: GB:L41145; NID:g755033; PID:g755034

C:Genetics:

A:Gene: BMP5

C:Superfamily: inhibin

Query Match 16.0%; Score 428; DB 2; Length 452;  
Best Local Similarity 29.0%; Pred. No. 1.1e-21;  
Matches 140; Conservative 66; Mismatches 164; Indels 112; Gaps 20;

QY 76 AKGCTGQT-----GGLTOPKKDEPKK-----LP--PRGCGPEPKCHPP-----QT 114

Db 25 AKGLGDNHVSIIYRLNRHERREITREILSLGLPHRPFSPGKQASSAPLFMLDL 84

QY 115 RQATARTVTPKGLP----GKAPPKAGSVSPFLKKAREPGPREPKEPRPPITPH 170

Db 85 YNAMASEDNPEYLVVSLAGEAKETRGYPASNGYAHRLHLPTLTQSP----- 140

QY 171 EYMLSLYRT--LSADRRKGNSSVKLEAGLANTITSIDKQDDRGVPVVRKQRYV---FD 225

Db 140 --LASLHDTNFDNDAD-----MVMSEFNLVERDKDFSHQRRHYKEFRFD 181

QY 226 ISAL-EXDGLLGAELRLRKPSDTAKPAAPGGGAAQ--LKLSSCPGROPAS----- 277

Db 182 LTQIPHGEAVTAAPFRIYKDK-----GNHRFENETIKIYQIITNRDADLF 231

QY 277 LLDVRSVPGLDGGGWEVFDI-----WKLFRNFKNSAQLCLEAWERGRAVDLRGLG-- 329

Db 232 LLDTRKQALD-VGWLVDITVTSNHWVINPONNLGLQLCAET---GDGRSINVKSAGLV 287

QY 329 -----FDRAARQVHEKALFLVFGRTKKRDLFTNEIKARSGQDDKVYIELFSQRR 378

Db 288 GRHGPOSKQPEWMAFFRASEVLLRSVRAASKRKQ--NRNKSNSHQDPS----- 335

QY 379 KRRLAPLATRQGRPSKNLKAQSKALHVNFKDMGWDWIIIAPLEYAFHCEGLCEPPLR 438

Db 335 --RMPSA---GDYNTSEQKQACKKHELYVSFRDLGWODWIIAPEGYAAFYCDGECSPFLN 389

QY 439 SHLEPTNHAIVQTLNMSMDPESTPTCCVPTRLSPISLTFLDSANNVYKQYEDMVVESC 498

Db 390 AHMNATNHAIVOTLVHLMFPDPVPRPCCAPTKLNAISLVLPFDSSNVLTKRYNNVVRSC 449

QY 499 GC 500

Db 450 GC 451

Search completed: October 31, 1999, 07:36:38

Job time: 2063 sec

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